

Run on:	November 20, 2002, 11:51:35	:	Search time 14:23:64	Seconds
	(without alignments)			
	1276.267 Million cell updates/sec			
Title:	US-09-658-699-2			
Perfect score:	1004			
Sequence:	1 MLGSRAVMLLLPWTAQGR.....QAFYAVAARVFAHGCNTLSP	189		
Scoring table:	BLOSUM62			
	Gpop 10.0	,	Gapext	0.5
Searched:	283224 seqs,	96134422 residues		
	total number of hits satisfying chosen parameters:			
	Minimum DB seq length:	0		
	Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
	Listing first 45 summaries			
Database :	PIR:73:*			
	1: pir1:*			
	2: pir2:*			
	3: pir3:*			
	4: pir4:*			
	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
	SUMMARIES			
Result No.	Query Score	Match Length	DB ID	Description
1	100	10.0	204	1 EQHUGL
2	99.5	9.9	194	2 TCGT55
3	91	9.1	208	1 S23549
4	80.5	9.0	174	2 T10268
5	88.5	8.8	207	2 A24573
6	87.5	8.7	208	2 A26496
7	86	8.6	1121	2 A32809
8	85	8.5	211	1 ICM56
9	80.5	8.0	232	2 D70537
10	80.5	8.0	530	2 A96810
11	80	8.0	858	2 JC7683
12	79.5	7.9	201	2 A42247
13	79	7.9	506	2 AG093
14	79	7.9	2512	1 XICHEA
15	78	7.8	1026	2 T05882
16	77.5	7.7	513	2 C82366
17	77.5	7.7	967	2 G86229
18	76.5	7.6	399	2 A11929
19	76.5	7.6	881	2 F84404
20	76	7.6	262	2 A84240
21	75.5	7.5	214	2 JC5043
22	75.5	7.5	265	2 B83395
23	75.5	7.5	938	2 A56731
24	75.5	7.5	2304	2 10790
25	75	7.5	195	2 I47070
26	75	7.5	211	2 A36247
27	75	7.5	901	1 S00943
28	75	7.5	975	2 T948107
29	74.5	7.4	212	2 I46621

interleukin 6 - pi				
hypothetical prote				
hypothetical prote				
hypothetical prote				
FL3K23.1B protein				
transcription-repa				
probable glucose-6				
probable glutamina				
probable glutanina				
photoreceptor - De				
beta-galactosidase				
testosterone-resis				
UDP-N-acetylglucosam				
class II histocomp				
oligopeptide ABC t				
	ALIGNMENTS			
	RESULT 1			
	EQHUGL			
	granulocyte colony-stimulating factor precursor - human			
	N;Alternate names: colony-stimulating factor 3; G-CSF			
	C;Species: Homo sapiens (man)			
	C;Date: 30-Jun-1998 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999			
	C;Accession: A25093; A49796; S68331			
	R;Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Kubota, N.; Oheda, M.			
	EMBO J 5, 575-581, 1986			
	A;Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-st			
	A;Reference number: A25093; MUID:86220137; PMID:2423327			
	A;Accession: A25093			
	A;Molecule type: DNA; mRNA			
	A;Residues: 1-204 <NAG>			
	A;Cross-references: EMBL:X03656; EMBL:X03655; PIDN:CAA27290.1; PID:973276			
	R;Devlin, J.J.; Devlin, P.E.; Myanbo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.			
	J;Leukoc. Biol. 41, 302-306, 1987			
	A;Title: Expression of granulocyte colony-stimulating factor by human cell lines.			
	A;Reference number: A49796; MUID:87196936; PMID:3494801			
	A;Accession: A49796			
	A;Molecule type: mRNA			
	A;Residues: 1-204 <DVS>			
	A;Cross-references: GB:MI1706; PID:9183040; PIDN:AAA35882.1; PID:9183041			
	R;Suza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Murdock, D.C.; Cha			
	Science 232, 61-65, 1986			
	A;Title: Recombinant human granulocyte colony-stimulating factor: effects			
	A;Reference number: A47587; MUID:86151684; PMID:2420009			
	A;Accession: A47587			
	A;Molecule type: mRNA			
	A;Residues: 1-1920 <SOU>			
	A;Cross-references: GB:MI3008; PID:9183044; PIDN:AAA03056.1; PID:9183045			
	R;Hiani, M.; Horan, T.; Arakawa, T.; Le, J.; Kaita, V.; Rohde, M.F.			
	Arch. Biochem. Biophys. 324, 344-356, 1995			
	A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.			
	A;Reference number: S68331; MUID:96132662; PMID:8554326			
	A;Accession: S68331			
	A;Molecule type: protein			
	A;Residues: M, 31-46 <HAN>			
	C;Genetics:			
	A;Gene: GDB:CSF3			
	A;Cross-references: GDB:119083; OMIM:138970			
	A;Map position: 17q11.2-17q12; 150/3			
	C;Function:			
	A;Description: stimulates the differentiation and proliferation of hematopoietic prog			
	C;Superfamily: Interleukin-6			
	C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer			
	F:1.3/Domain: signal sequence #status predicted <SIG>			
	F:31/204/Domain: granulocyte-colony stimulating factor #status predicted <MRN>			
	F:66-72/94-104/Disulfide bonds: #status predicted			

Page 3

C;Genetics:	
A;A;Introns: 14/1; 71/3; 107/3; 156/3	
C;Superfamily: interleukin-6	
C;Keywords: cytokine; growth factor; monomer	
Query Match 36 LSOKLCTLAWSAHP-----LIVGMDLUREEDEETINDYPIQCGDGCDCPQGLRDNSQFCLOQ 91	Score 87.5; DB 2; Length 208;
Best Local Similarity 25.0%; Pred. No. 0.78; Mismatches 59; Indels 41; Gaps 10;	
Matches 41; Conservative 23; Mismatches 59; Indels 41; Gaps 10;	
Db 67 LLSQCATYKLUPEEDVLGLH-----SLGPKASL-SGESSQAAQTTQ-QCLS 112	
Qy 92 RIHGLIFYEKGLSDIFTG-EPSLLPDSPVQAHLAS-----LIGLSQLI.QPEG 139	
Db 113 QIUSGLCLYQQGL---QALSGISPAALPTDLIQDVAFTIWIQWQENLGVAPPVQP-- 168	
Qy 140 HWHETQQ-IPSLSQSPWQRLPLREKILSQAFTAVANARVFAH 182	
Db 169 ---TQSAMPATSA-FQRAGGYLAIYSQGLFETARLHH 206	
RESULT 7	
A82809 A82809 exodeoxyribonuclease V gamma chain XFO422 (imported) - <i>Xylella fastidiosa</i> (strain 9a... C;Species: <i>Xylella fastidiosa</i> C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 C;Accession: A82809 C;Anonymous, The <i>Xylella fastidiosa</i> Consortium of the organization for Nucleotide Se... Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant Pathogen <i>Xylella fastidiosa</i> . A;Reference number: A82515; PMID:20365117; PMID:1091047 A;Accession: A82809 A;Note: for a complete list of authors see reference number A59328 below A;Status: preliminary A;Molecule type: DNA A;Cross-references: GB:AEO03899; GR:AE003849; NID:99105253; PIDN:AAF83232.1; GSPDB:Gr A;Experimental source: strain 9a5C R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencento, M.; Alvarenga, R Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.B.; Camargo, L.E.A.; Carraro, D.M.; Carreto, A; Authors: Martins, E.M.F.; Madeira, A.M.B.N.; Marinho, C.L.; Marques, M.V.; Martinez-Aroso, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, J.A.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, S.C.; Franca, M.C.; Funchal, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Lachado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martinez-Aroso, B.; Oliveira, M.K.A.; Oliveira, M.C.; Oliveira, R.C.; Miyaki, C.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.G.; Santelli, S.; Sawa, F.G.; Nunes, L.R.; Oliveira, M.C.; de Rosa Jr., V.E.; de Sa, R.G.; Tsuchiko, M.H.; Valada, da Silva, F.R.; da Silva, A.M.; Silva Jr., W.H.; da Silva, A.P.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.H.; da Silva, M.H.; Valada, H.; van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A;Reference number: A59328 A;Contents: annotation C;Genetics:	
A;Gene: XFO422	
Query Match 22 VPGGSSPAWTQCCQLSOKL----CTL-----ANSA-----HPLVGHMDLREFGDE 62	Score 86; DB 2; Length 1121;
Best Local Similarity 23.7%; Pred. No. 8; Mismatches 56; Indels 58; Gaps 9;	
Matches 41; Conservative 18; Mismatches 56; Indels 58; Gaps 9;	
Db 236 LPPTKEWGDAQPTORLHPDTCYQTQENRILHANGAAGIDFMVGLSYEVWIPSGE 295	
Qy 63 ETNDVPHIQLQCGDQCDPQGLRDNSQFCLOQRIHQGLIFYEKLGSDIFTGE---PSLLP- 117	
Db 296 ITAYDFFQRLGTLDGLGRDS---LLQRMH-----ADLFHNRSAPVAPPLPA 341	
Qy 118 ---DPSVQAHLSLGSQQLSOKL-----OPEGHWHWTQQFQPSLSRSQ 154	
Db 342 PRJEDPSLQFHACTRLRELQYHDLRALLEPPNSPEQRFN---BPLQPRE 390	

RESULT 8

TCMS6
Interleukin-6 precursor - mouse
 ; Alternative names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte acytoma growth factor
 ; Species: Mus musculus (house mouse)
 ; Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999
 ; Accession: A30531; A27610; A30531; S01323; S12103; E34017; A26662; A0486; A60799; S10
 ; R: Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
 ; J. Immunol. 141, 3875-3881, 1988
 ; A: Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential cDNA cloning of murine interleukin-6P1: homology with human interleukin 6.
 ; A: Reference number: A30531; MUID:89035525; PMID:3263439
 ; A: Accession: A30531
 ; A: Molecule type: DNA
 ; A: Residues: 1-211 <TAN>
 ; A: Cross-references: GB:M20572; PIDN:9198369; PIDN:AAA39302.1; PMID:9387386
 ; R: Van Snick, J.; Cyphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
 ; Eur. J. Immunol. 18, 193-197, 1988
 ; A: Title: cDNA cloning of murine interleukin-6P1: homology with human interleukin 6.
 ; A: Reference number: A27610; MUID:88166883; PMID:2965020
 ; A: Accession: A27610
 ; A: Molecule type: mRNA
 ; A: Residues: 1-211 <YAN>
 ; A: Cross-references: GB:X06203; PID:952701; PIDN:CAA29560.1; PMID:952702
 ; R: Mock, B.A.; Nordan, R.P.; Justice, M.J.; Rozak, C.; Jenkins, N.A.; Copeland, N.G.; Cle
 ; J. Immunol. 142, 1372-1376, 1989
 ; A: Title: The murine Il-6 gene maps to the proximal region of chromosome 5.
 ; A: Reference number: A30571; MUID:89124383; PMID:2563387
 ; A: Accession: A30571
 ; A: Molecule type: mRNA
 ; A: Residues: 5-211 <MOC>
 ; R: Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 ; Eur. J. Biochem. 176, 187-197, 1988
 ; A: Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and r
 ; A: Reference number: S01323; MUID:88329059; PMID:3262059
 ; A: Molecule type: protein
 ; A: Residues: 25-166 'X' 168-211 <SIM>
 ; A: Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 ; R: Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
 ; Nucleic Acids Res. 18, 6455, 1990
 ; A: Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 ; A: Reference number: S12103; MUID:91057159; PMID:2243807
 ; A: Molecule type: mRNA
 ; A: Residues: 1-211 <GRE>
 ; R: Jannen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
 ; Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 ; A: Title: Internal amino acid sequencing by *in situ* cyanogen bromide cleavage
 ; A: Reference number: A90157; MUID:90147691; PMID:3202197
 ; A: Accession: E34047
 ; A: Molecule type: protein
 ; A: Residues: 66-69, 'X' 71-75-'94-'148 <JA5>
 ; R: Van Snick, J.; Cyphas, S.; Vink, A.; Uttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simp
 ; Proc. Natl. Acad. Sci. U.S.A. 81, 9679-9683, 1986
 ; A: Title: Purification and NH₂-terminal amino acid sequence of a T-cell-derived lymphokin
 ; A: Reference number: A26662; MUID:87092311; PMID:2448184
 ; A: Molecule type: protein
 ; A: Residues: 25-39, 'X' 41-42, 'X' 44-45 <VSN>
 ; R: Chiu, C.P.; Mouls, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 ; Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 ; A: Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 ; A: Reference number: A40486; MUID:89017145; PMID:3262872
 ; A: Accession: A40486
 ; A: Molecule type: mRNA
 ; A: Residues: 1-211 <CHI>
 ; R: Shao, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 ; Blood 72, 2070-2073, 1988
 ; A: Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6

RESULT 9

D70537
hypothetical protein Rv1115 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998
C:Accession: D70537
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A:Authors: Sopres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:9839587; PMID:9634230
A:Accession: D70537
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-232 <COL>
A: Cross-references: GB:295585; GB:AL123456; NID:93261787; PMID:CA80947.1; PID:e31713
A: Experimental source: strain H37RV
C:Genetic: Kv11.5
A:Gene: Kv11.5

A: Reference number: A60799; MUID:890622753; PMID:3264198
A: Accession: A60799
A: Molecule type: protein
A: Residues: 77-98 <SHA>
R: Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A: Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a
A: Status: preliminary
A: Reference number: S10241
A: Accession: S10241
A: Molecule type: DNA
A: Residues: 1-6 <HLA>
A: Cross-references: EMBL:X51457; PIDN:CAA35824.1; PID:9584860
R: Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A: Title: Specific covalent modification of the tryptophan residues in murine interleukin-6
A: Reference number: S38254
A: Accession: S38254
A: Status: preliminary
A: Molecule type: protein
A: Residues: 38-60/75, X, 77-79, 176-203 <ZHA>
C:Genetics:
A: Gene: IL-6
A: Map position: 5
A: Introns: 7/1; 68/3; 106/3; 156/3
C: Superfamily: interleukin-6
C: Keywords: Castelman's disease; cytokine; growth factor; immunoregulation; lymphokin
P: 1-24/Domain: signal sequence #status predicted <SIG>
F: 25-211/Product: interleukin-6 #status experimental <MAT>
Query Match Score 85: DB 1; Length 211;
Matches 44; Conservative 20; Mismatches 58; Indels 70; Gaps 9;
QY 28 PAWTCQCDPGLRDNQSFCQRHFGLFFY-----KLGSD-----KLIGSD----- 108
Db 44 PVYTISQVGGGLTHVLNEVMRKELCN-----GNSDCMNNDAAENNLKPEIQ 94
QY 73 CGGCCDPGLRDNQSFCQRHFGLFFY-----KLGSD-----KLIGSD----- 108
Db 95 RNDDQCYQGY--NQEICQLKSSGLLEYSYLEYMKNNLDKNDKDKARVQLQRDTETLII 152
QY 109 FTGEPSSLPDSPVQAHLASLL-GLSQLQPEGHHWETQPSLSPQWLRLRFKIL 166
Db 153 FNQE-----VKDHLKIVLPPTSNALTD-----KLESQKEWLRLKTIQFL 194
QY 167 RSLODAFVVAAR 178
Db 195 KSLEEFKVTLR 206

Query Match	8.0%	Score 80.5; DB 2; Length 232;	A;Residues: 1-858 <KIT>
Best Local Similarity	23.4%	Pred. No. 4;	A;Cross-references: DDBJ:AB049994
Matches	49;	Conservative 27; Mismatches 68; Indels 65; Gaps 11;	C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of gene expression.
'	9	LLLPLPWTQAGRYPGGSSPAWTQCOQLSQLCLTLAWSAHPLYGHMDLREEGDEE---- 63	C;Genetics:
'	26	LLTLINQVIGTPYPGGSPAGTDCSERLAWNRA-TARPVFG--DRFTNGNEEAALA 82	A;Gene: tlr3
'	64	-----TTNDYPHIQCGDCDPOGLRDNSONCQLRTHQGLIFY 100	A;Map position: 4
'	83	RGFQGTAPNALVIGWNGHTAVLPDGTPVSSGBG--GGVRYGG--GGYQPKFTH 135	C;Keywords: transmembrane protein
'	101	EKLGSIDTEGE--PSLQPSVAQHSLASLGLSQQPSQ---- 154	Query Match
'	136	HNYLPMVDAGEDOPPA-PDEPVATPD-----VEPE-----MPADCPTORPP 177	Best Local Similarity 8.0%; Score 80; DB 2; Length 858;
'	155	--PWQRLLRKFL-RSLQAFYAAVAF 180	Pred. No. 21; Mismatches 9; Gaps 11;
'	178	VTPRNLCNRRLRTMPGALSAALAAAAPW 206	Matches 51; Conservative 9;
RESULT 10			Mismatches 66; Indels 60; Gaps 11;
'	366810	hypothetical protein T1111_6 (imported) - Arabidopsis thaliana	A;Map position: 4
'		Species: Arabidopsis thaliana (mouse-ear cress)	C;Keywords: transmembrane protein
'		Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001	C;Cross-references: NCBI:3333
'	D96810	Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, R.; Hwang, N.F.; Hughes, B.; Huizar, L.	C;Accession: D96810
'		Nature 408, 816-820, 2000	C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
'		Authors: Hunter, J.L.; Jenkins, J.; Johnson Hopson, C.; Khan, S.; Kharkin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzali, N.; Rooney, T.; Rowley, D.; Sakano, H.	C;Species: Gallus gallus (chicken)
'		Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	C;Accession: A42247; S06633
'		critique, M.; Hughes, B.; Huizar, L.	R;Sternbeck, E.; Blattner, C.; Graf, T.; Leutz, A.
'		Sequence number: A86141; MUID:21016719; PMID:11130712	Mol. Cell. Biol. 12, 1728-1735, 1992
'		Reference number: 42247; MUID:92195319; PMID:1549124	A;Title: Structure of the chicken myelomonocytic growth factor gene and specific A;Reference number: A42247; MUID:92195319; PMID:1549124
'		Status: preliminary	A;Accession: A42247
'		Molecule type: DNA	A;Status: preliminary
'		Cross references: GB:AE005173; NID:96587860; PIDN:CAA32639.1; PIDN:CA32639.1; PIDN:963596	A;Molecule type: DNA
'		Genetics: T1111_6	A;Residues: 1-201 <STRE>
'		Map position: 1	A;Note: sequence extracted from NCBI backbone (NCBIN:89832; NCBI:89836)
'		Genetics: T1111_6	R;Leutz, A.; Damm, K.; Sternbeck, E.; Ness, S.; Frank, R.; Gausepohl, H.;EMBO J. 8, 175-181, 1989
'		Map position: 1	A;Title: Molecular cloning of the chicken myelomonocytic growth factor (cM-CSF); Reference number: S03633; MUID:89231616; PMID:2785450
'		Genetics: T1111_6	A;Molecule type: mRNA
'		Map position: 1	A;Residues: 1-201 <LEU>
'		Genetics: T1111_6	A;Cross-references: EMBL:X14477; NID:963596; PIDN:CAA32639.1; PID:963597
'		Map position: 1	C;Superfamily: interleukin 6
'		Genetics: T1111_6	C;Keywords: glycoprotein
'		Map position: 1	F;1-23/Domain: signal sequence #status predicted <SIG>
'		Genetics: T1111_6	F;24-201/Product: myelomonocytic growth factor #status predicted <MAT>
'		Map position: 1	F;123-137/Binding site: carbohydrate (Asn) (covariant) #status predicted
'		Genetics: T1111_6	Query Match
'		Map position: 1	Best Local Similarity 7.98%; Score 79.5; DB 2; Length 201;
'		Genetics: T1111_6	Mismatches 19; Pred. No. 4.2; Gaps 19;
'		Map position: 1	Matches 36; Conservative 19;
'		Genetics: T1111_6	Mismatches 52; Indels 19; Gaps 6;
'		Map position: 1	Accession: T1111_6
'		Genetics: T1111_6	Query Match
'		Map position: 1	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Genetics: T1111_6	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Map position: 1	Matches 28; Conservative 22; Mismatches 38; Indels 21; Gaps 6;
'	Y	78 DPQGLR--DNSQFLCQLRTHQGLIFYKLLGSDIFTGEPSSLPDSPV--AQHLASLLGLIS 133	Query Match
'	b	158 DPETLKKMGNEYCRGRFOALFYERISAD-----PKPTPYWSKKSAAALISLR 208	Best Local Similarity 25.7%; Score 80.5; DB 2; Length 530;
'	Y	134 LIQPEGHWHETQOQLPSLPSOPWORLLRFKFLRSLOAFYAAVAFH 182	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'	b	209 LLEASD--ACEEALRNP---YERAHR--LASTLQLRGEVERKALCH 249	Matches 28; Conservative 22; Mismatches 38; Indels 21; Gaps 6;
RESULT 11			Accession: T1111_6
'	CY7683	transmembrane receptor T1111_6	Query Match
'		species: Mus musculus (house mouse)	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Accession: JC7683	Accession: JC7683
'		Biophys. Res. Commun. 283, 236-242, 2001	Query Match
'		Reference number: JC7683; MUID:21222875; PMID:11322794	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Comments: tongue	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Accession: JC7683	Accession: JC7683
'		Molecule type: DNA	Query Match
'		Cross references: NCBI:3333	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Genetics: T1111_6	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Map position: 1	Accession: T1111_6
'		Genetics: T1111_6	Query Match
'		Map position: 1	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Genetics: T1111_6	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	Query Match
'		Genetics: T1111_6	Best Local Similarity 8.0%; Score 80.5; DB 2; Length 530;
'		Map position: 1	Pred. No. 11; Mismatches 28; Indels 21; Gaps 6;
'		Genetics: T1111_6	Accession: T1111_6
'		Map position: 1	

Db	192 YRALRH 197	
RESULT 13		
AG0893	aerotaxis receptor protein [imported] - <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi	
C;Species:	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi	A;Note: this species has also been called <i>Salmonella typhi</i>
C;Date:	09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002	
C;Accession:	AG0893	
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulie, S.; O'Gaora, P.	Nature 413, 848-852, 2001	A;Title: Amino acid sequences of substrate-binding sites in chicken liver fatty acid synthase CDNA.
A;Authors:	Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;	A;Reference number: AB0502; PMID:11677608
A;Accession:	AG0893	A;Residues: 75-77, 'PV', 80-116, 'A', 118-675, 'S', 677-1169, 'N', 1171-1178, 'T', 1180-1191, 'H
A;Status: preliminary		A;L>
A;Molecule type: DNA		A;Accession: A30445
A;Residues: 1-506 <PAR>		A;Molecule type: protein
A;Cross-references: GB:AL513382; PIDN:CAD07741.1; PID:g16504293; GSPDB:GN00176		A;Residues: 107-113,1086-1091 <HOLL>
C;Genetics:		R;Juan, Z.; Liu, W.; Hammes, G.G.
C;Gene:	SYN3395	Proc. Natl. Acad. Sci. U.S.A. 86, 4387-4391, 1989
C;Superfamily: methyl-accepting chemotaxis protein		A;Title: Molecular cloning and sequencing of chicken liver fatty acid synthase
Qy	4B HPLVGHMDI-----REEGDE--ETNDVPHIQCGDGCQF 80	A;Reference number: A33918; MUID:89282777; PMID:2734291
Db	53 HNLVRHPDPKAAFDAMWYTLKOGPEPMGSIVNRNRNGDHHWVRANAVAPIREGRVGYM 112	A;Accession: A31236
Qy	81 GLRD-----NSQFCQLQRHGLIFYKEKLIGSDIFTGEPSLIPDPSVQAQ 123	A;Residues: 1752-2512 <YUA2>
Db	113 SIRTRATDEIAAVEPILYQALNEGRCSKRHKLVYRQGLGK-----LPAMPYRW 163	A;Cross references: GB:J03860; GB:M22987; NID:9211766
Qy	124 LHASLLGLSQLLOPPEGHWETQOIPSLSPSQFWQRLL-----RFKFLRSQ 171	A;Note: neither the complete nucleic acid sequence nor the complete translation are s
Db	164 RVRSIMGLMAVM-----LALALFGTDASWQALLGALMLAGTALPEWQTVRPIEN 214	R;Chirala, S.S.; Kasturi, R.; Pazirandeh, M.; Stolow, D.T.; Huang, W.Y.; Wakil, S.J.
Qy	172 FVAVAARV 179	A;Title: A novel cDNA extension procedure. Isolation of chicken fatty acid synthase c
Db	215 VATQALKV 222	A;Reference number: A30297; MUID:89139426; PMID:2917973
RESULT 14		
XCHFA	enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific) (EC 1.3.1.10) - chicken	A;Accession: A31184
N;Contains:	3-hydroxypalmitoyl-1-acyl-carrier-protein] dehydratase (EC 4.2.1.61); 3-oxoacyl-1-acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.10); oleoyl-[acyl-car	A;Molecule type: protein
C;Species:	protein] S-malonyltransferase (EC 2.3.1.39)	A;Residues: 2209-2508 <YAN>
C;Accession:	Gallus gallus (chicken)	R;Kasturi, R.; Chirala, S.; Pazirandeh, M.; Wakil, S.J.
C;Date:	30-Sep-1991 #sequence_revision 12-Apr-1996 #text_change 03-Jun-2002	Biochemistry 27, 7778-7785, 1988
C;Accession:	S57248; S51519; A30620; A29967; A33918; A30445; A31236; A31236; A31	A;Title: Characterization of a genomic and cDNA clone coding for the thioesterase dom
R;Huang, W.Y.; Chirala, S.S.; Wakil, S.J.	ain in F19. 5	A;Reference number: A31185; MUID:8908152; PMID:3207710
subunit to the EBLB Data Library, January 1989	R;Huang, W.Y.; Stoops, J.K.; Wakil, S.J.	A;Accession: A31185
A;Description: Amido-terminal blocking group and sequence of the animal fatty acid synthase	Arch. Biochem. Biophys. 270, 92-98, 1989	A;Molecule type: mRNA
A;Accession number: S57248	A;Title: Complete amino acid sequence of chicken liver acyl carrier protein derived f	A;Residues: 2202-2512 <KAS2>
A;Accession:	A;Reference number: S51519; MUID:95031085; PMID:7944406	A;Reference number: S03556
A;Molecule type: mRNA	A;Accession:	A;Molecule type: protein
A;Residues: 1-182 <HU42>	R;Chang, S.J.; Hammes, G.G.	A;Residues: 2121-2209 <HU44>
A;Cross-references: EMBL:J04485; PID:9460908; PIDN:AAB46389.1; PID:g460907	Biochemistry 28, 3781-3786, 1989	A;Cross-references: EMBL:J02839; NID:9211768
A;Accession:	A;Title: Amino acid sequences of pyridoxal 5'-phosphate binding sites and fluorescen	A;Accession: A30620

A; Reference number: A32015; MUID:89323081; PMID:2751995
 A; Accession: A32015
 A; Molecule type: protein
 A; Residues: 667-675; 1639-1709 <CHA2>
 A; Note: the binding of pyridoxal 5'-phosphate to Lys-1708 competitively inhibits the bin
 C; Function: <HPD>
 A; Description: as 3-hydroxyalmitoyl [acyl-carrier protein] dehydratase (EC 4.2.1.61) ca
 A; Pathway: fatty acid biosynthesis
 A; Note: this activity is specific for C12 to C16 acyl compounds
 C; Function: <OAR>
 A; Description: as 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) catalyzes th
 -[acyl-carrier-protein] and NADP+
 A; Pathway: fatty acid biosynthesis
 C; Function: <OAS>
 A; Description: as 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) catalyzes the
 acyl-carrier-protein, acyl-carrier-protein and carbon dioxide
 C; Function: <BAR>
 A; Description: as enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.1)
 [acyl-carrier-protein] and NADP+
 A; Pathway: fatty acid biosynthesis
 C; Function: <HYD>
 A; Description: as oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) catalyzes the hy
 A; Pathway: fatty acid biosynthesis
 C; Function: <SAT>
 A; Description: as [acyl-carrier-protein] S-acetyltransferase (EC 2.3.1.38) catalyzes the
 Acyl-A
 C; Function: <SMR>
 A; Description: as [acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) catalyzes th
 enzyme A
 A; Pathway: fatty acid biosynthesis
 C; Superfamily: rat fatty acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homo
 ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S
 C; Keywords: acetylated amino end; acyltransferase; alternative splicing; carbon-oxygen
 P; Oxidoreductase; phosphopentetheine; phosphoprotein; thiolester hydrolase
 F; 1-2512/Product: fatty acid synthase, splice form 1 #status predicted <MAT1>
 F; 1-2350, CFSFLQFQ, 2351-2512/Product: 3-oxoacyl-[acyl-carrier-protein] synthase, splice form 2 #status predicted
 F; 22-404/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASH>
 F; 492-774/Domain: [acyl-carrier protein] S-malonyltransferase homology <ANT>
 F; 1322-1340/Region: catalytic (3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase)
 F; 1554-1838/Region: long-chain alcohol dehydrogenase homology <ADH>
 F; 1675-1704/Region: beta-alpha-beta NADP nucleotide-binding fold
 F; 1888-2070/Region: short-chain alcohol dehydrogenase homology <SDADH>
 F; 2234-2487/Domain: acyl carrier protein homology <ACPH>
 F; 1/Modified site: acetylated amino end (Met) #status experimental
 F; 161/Active site: Cys #link OAS #status predicted
 F; 1705,1708/Active site: Ser #link SAT, SMT #status predicted
 F; 1930/Active site: Lys #link OAR #status predicted
 F; 2158/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
 F; 2309/Active site: Ser #link HYD #status predicted

Query Match 7.9%; Score 79; DB 1; Length 2512;
 Best Local Similarity 23.3%; Pred. No. 95;
 Matches 37; Conservative 23; Mismatches 51; Indels 48; Gaps 9;

Qy 20 RAVPGGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREECDEETNDVPHIQCGDCP 79
 Db 1170 KGAAAGSPPAQKGQLQHITELICRELNGNP---HSED---EQIVIQERKHLQ---DDP 1218

Qy 80 -QGIRDNSOF-CLQRHQG----LIFYEKLGSDFTEKAKNTSHRMKIVEALAGSCLRFSRVQSTINTQPLQLDYIAF 123
 Db 1219 LLNLGLDSSSLKTCIDVAKENTSHRMKIVEALAGSCLRFSRVQSTINTQPLQLDYIAF 1278

Qy 124 -----LHASLIGLSQOLQPQGHMKTQQLPS 149
 Db 1279 DCTPTEIISDNETEIHDAQSISFSQ-----WDPSSU 1309

* GenCore version 5.1.3
 Copyright (c) 1993 - 2002 Compugen Ltd.

 4 protein - protein search, using sw model
 run on: November 20, 2002, 11:48:59 ; Search time 7.85455 Seconds
 (without alignments)
 998.024 Million cell updates/sec

 title: US-09-658-699-2
 perfect score: 1004
 sequence:
 1 MLGSRVAMILLILPWTQGR.....QAFVAAARVFAHGAATLSP 189

Scoring table: BLOSUM62
 Gapopen 10.0 , Gapext 0.5
 112892 seqs, 41476328 residues
 Total number of hits satisfying chosen parameters: 112892
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0.8%
 Maximum Match 1.00%
 Listing first 45 summaries
 SwissProt 40 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ESTIMABILITY

CONTINUOUS

Result No.	Score	Query Match	Length	DB ID	Description	
					DB	ID
1	106.5	10.6	195	1	CSF3_PIG	002837 suis scrofa
2	96.5	9.9	194	1	CSF3_FELCA	002078 felis silve
3	96	9.6	208	1	IL6_SHEEP	P29455 ovis aries
4	90.5	9.0	174	1	CSF3_SHEEP	P28746 ovis aries
5	89.5	8.9	175	1	CSF3_CANFA	P35834 canis famili
6	89	8.9	208	1	IL6_APPI	P28819 capra hircu
7	88.5	8.8	207	1	CSF3_HUMAN	P05919 homo sapien
8	87.5	8.7	208	1	CSF3_MOUSE	P05920 mus musculus
9	85	8.5	211	1	IL6_MOUSE	P08505 mus musculus
10	80.5	8.0	195	1	CSF3_BOVIN	P35833 bos tauru
11	80.5	8.0	581	1	FRZ3_DROME	077438 drosophila
12	79.5	7.9	201	1	MGF1_CHICK	P13854 gallus galli
13	79	7.9	2511	1	FAS_HICK	P12716 gallus galli
14	78.5	7.8	208	1	IL6_FELCA	P141683 felis silv
15	78.5	7.8	450	1	AT10_MOUSE	P58459 mus musculus
16	77.5	7.7	513	1	RMUC_VIRCH	Q9K97 vibrio chol
17	75.5	7.5	938	1	CAFA_HUMAN	Q13160 homo sapien
18	75	7.5	205	1	IL6_ORCOR	P28747 orcinus orca
19	75	7.5	211	1	IL6_RAT	P20607 rattus norv
20	75	7.5	801	1	DHGA_ACICA	P05465 acinetobacte
21	74.5	7.4	212	1	IL6_PIG	P26593 suis scrofa
22	73.5	7.3	201	1	TNFB_MACEU	09X148 macropus eeu
23	73.5	7.3	207	1	IL6_CANFA	P41323 canis famili
24	73.5	7.3	247	1	6PGL_MYCTU	006614 mycobacteri
25	73.5	7.3	755	1	BPHY_DETRIA	Q9ZCA4 deinococcus
26	73.5	7.3	1015	1	BGAL_ARISP	Q59140 arthrobacte
27	72	7.2	501	1	KG3H_DRONE	P83101 asperochilia
28	71.5	7.1	310	1	GLS1_ECOLI	P77454 escherichia
29	71	7.1	208	1	IL6_BOVIN	P26592 bos tauru
30	71	7.1	212	1	IL6_CERTO	P46550 cercopibus
31	71	7.1	483	1	KPKY_METEX	005118 myellobacte
32	71	7.1	619	1	ELFL1_HUMAN	P37790 homo sapien
33	70	7.0	105	1	TND1_HUMAN	P37790 homo sapien

34	70	7.0	427	1	THIL_HUMAN	P24752	homo sapien
35	70	7.0	726	1	ADD_HUMAN	Q43506	homo sapien
36	70	7.0	812	1	PDALORYSA	Q43007	oryza sativ
37	70	7.0	1538	1	LHR_ECOLI	P30015	Escherichia
38	69.5	6.9	208	1	TL6_HORSE	P00181	equus cabal
39	69.5	6.9	430	1	KDTA_CHLMU	Q9PK5	chlamydia m
40	69.5	6.9	514	1	G6PD_MYCTU	Q08407	mycobacteri
41	69.5	6.9	1396	1	VCPA_VZVD	P09245	varicella-z
42	69.5	6.9	1544	1	TUSP_HUMAN	Q9nrj4	homo sapien
43	69	6.9	234	1	NK4_HUMAN	P24001	homo sapien
44	69	6.9	592	1	FTS2_BARBA	O31314	bartoneill
45	69	6.9	639	1	AMYG_ASPAK	P23176	asneroillus

ASSIGNMENTS

RESULT_1
CSF3_PIG
ID CSF3_PIG
AC C02927_C19190
STANDARD:
PRT;
195 AA.

DT 12-JUL-1998 rel. 39 Last sequence update
 DT 30-MAY-2000 rel. 39 Created
 DT 15-JUN-2002 rel. 39 Last annotation update
 DE Granulocyte colony stimulating factor precursor (G-CSF).

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eute-

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TAXID=9823;

RA SEQUENCES FROM N.A.
KU Kulmburg P.
RE

RL Submitted (JAN-1997) to the EMBL/GenBank/DDJB databases.

RP SEQUENCE FROM N.A.
 TISSUE=Liver;
 RC Gloster S.D., Sandeman R.M., Strom A.D.G.;
 RA "Cloning of a cDNA and gene encoding porcine granulocyte-colony
 stimulating factor";
 RT Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RL CYTOKINES THAT ACT IN HEMATOPOIETICALLY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
 CC CSF INDUCES GRANULOCYTES BY SIMILARITY .
 CC -1-
 CC SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secretoin.
 CC -1- PTM: O-GLYCOSYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on
 CC use by non-profit institutions as long as its content is in no
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: Y10494; CAA71518.1; -.
 DR EMBL: U68482; AAB70701.1; -.
 DR EMBL: U68481; AAB70700.1; -.
 DR HSSP: P35833; 1BGC;
 DR InterPro: IPR003629; GCSF_MGF .
 DR InterPro: IPR003573; IL6_MGF_GCSF .
 DR Pfam: PF00489; IL6_1.
 DR PRINTS: PR00433; IL6GCSMGF .
 DR PRODOM: PD008388; GCSF_MGF .
 DR SMART: SM00126; IL6_MGF .
 DR PROSITE: PS00254; INTERLEUKIN_6_1.
 KW Cytokine; Growth factor; Glycoprotein; Signal .
 ET SIGNAL .
 CHAIN 1
 CHAIN 22 195
 CHAIN 22 195

PROSITE; PS00254; INTERLEUKIN_6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.

FT DISULFID 57 63 BY SIMILARITY.
 FT DISULFID 85 95 BY SIMILARITY.

FT CARBOHYD 154 154 O-LINKED (GALNAC. . .) (BY SIMILARITY).

FT CONFLICT 123 123 A -> R (IN REF. 1).

FT SEQUENCE 195 AA; 21214 MW; 84787F2DB0AEAC CRC64;

Query Match 10.6%; Score 106.5; DB 1; Length 195;
 Best Local Similarity 24.9%; Pred. No. 0.0044; Gaps 10;
 Matches 52; Conservative 28; Mismatches 76; Indels 53; Gaps 11;

Qy 7 VMLLILPWTQAGRAVPGGS -SPAWTQCO-----QLSQQLCLAWS 46
 Db 3 LMLQLLWHLALWMPPEAPLSPASSPLPSFLKCLEQVRKIQADGAEIQLCATHKL 62

Qy 47 AHP ---LVGHMDLRREGDEETNDYPHICGDDPOGLRDSOFLCQLRHQGLIFYEK 102
 Db 63 CHFOELVLLGH -----SGLQPASL-SSCQSSQALQLTG-CLNQGLGGLYQG 108

Qy 103 LGSDIFTG-EPSLIPDPSVPAQLHSLGLSQLLOPEGHWWETQQIPSLPSQ-----154
 Db 109 LL-QALAGISPEKLLRSLOAFVAVAARYFAH 182

Qy 155 -PNORLILRKFLRSLOAFVAVAARYFAH 182

Db 163 SAFORRAGGVVVQSOLSELAYRLY 191

RESULT 2
 CSF3_FELCA STANDARD PRT; 194 AA.

ID CSF3_FELCA STANDARD PRT; 194 AA.
 AC 002208;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
 GN CSF3.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1] NCBI_TAXID=9655;

RP SEQUENCE FROM N.A.
 RA STRAIN=European shorthair; TISSUE=Lung;
 RA Dunham S.P.; Onions D.E.;
 RT "Cloning, sequencing and expression of feline granulocyte colony
 stimulating factor."
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOEISIS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
 CC CSF INDUCES GRANULOCYTES (BY SIMILARITY),
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL; Y08558; CAA67858; 1. -.
 DR HSSBL; P35634; 1BGE.
 DR InterPro; IPR003629; GCSE_MGF.
 DR InterPro; IPR005753; IL6_MGF_GCSF.
 DR Pfam; PF0489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSE_MGF; 1.
 DR SMART; SR00126; IL6; 1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.

FT NON_TER 1 1 POTENTIAL.
 FT SIGNAL <1 20 GRANULOCYTE COLONY-STIMULATING FACTOR.

FT CHAIN 21 194 BY SIMILARITY.

FT DISULFID 56 62 BY SIMILARITY.

FT CARBOHYD 84 94 O-LINKED (GALNAC. . .) (BY SIMILARITY).

FT SEQUENCE 153 153 BY SIMILARITY.

Query Match 9 9%; Score 99.5; DB 1; Length 194;
 Best Local Similarity 23.9%; Pred. No. 0.02; Matches 50; Conservative 27; Mismatches 79; Indels 53; Gaps 11;

Qy 7 VMLLILPWTQ---GRAVPGGSPPAWO---C00-----LSQKLUCLAWS 46
 Db 2 LMLQLLWHLALWMPPEAPLSPASSPLPSFLKCLEQVRKVOADGDTALQERLCAAHKL 61

Qy 47 AHP ---LVGHMDLRREGDEETNDYPHICGDDPOGLRDSOFLCQLRHQGLIFYEK 102
 Db 62 CHPPEELVIGH-----ANGIPQAPI-SSCSSLQALQTG-CLRQHSGGFLYQG 107

Qy 103 LGSDIFTG-EPSLIPDPSVPAQLHSLGLSQLLOPEGHWWETQQIPSLPSQ-----154
 Db 108 LL-QALAGISPEKLLRSLOAFVAVAARYFAH 182

Qy 155 -PNORLILRKFLRSLOAFVAVAARYFAH 182

Db 162 SAFQRAGGTIVASNLQSLEVATRALRH 190

RESULT 3
 IL6_SHEEP STANDARD PRT; 208 AA.

ID IL6_SHEEP ID P2455;
 AC 01-APR-1993 (Rel. 25, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-6 precursor (IL-6).
 DE NCBITAXID=9940;
 GN Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccra; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1] RP SEQUENCE FROM N.A.
 RX MEDLINE-9401419; PubMed=8225400;
 RA Andrews A.E.; Barcham G.J.; Ashman K.; Meeusen E.N.T.; Brandon M.R.; Nash A.D.;
 RA "Molecular cloning and characterization of a ruminant interleukin-6 precursor."
 RT CDNA;
 RT RNA;
 RL Immunol. Cell Biol. 71:341-348(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ebrahimi B.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL; Y08558; CAA67858; 1. -.
 DR HSSBL; P35634; 1BGE.
 DR InterPro; IPR003629; GCSE_MGF.
 DR InterPro; IPR005753; IL6_MGF_GCSF.
 DR Pfam; PF0489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR ProDom; PD008388; GCSE_MGF; 1.
 DR SMART; SR00126; IL6; 1.

DR EMLL; X62501; CAA44363.1; .
 DR DR; X68723; CAA48652.1; .
 DR EMBL; A19159; CAA01443.1; .
 DR PIR; S29549; S29549.
 DR PIR; P05231; IL16.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00483; IL6; 1.
 DR PRINTS; PRO0433; IL6GCSFMGF.
 DR PRODOM; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SIGNAL; 1; 29.
 KW CYTOKINE; Glycoprotein; Growth factor; Signal.
 FT SIGNAL; 1; 29.
 FT CHAIN; 30; 208.
 BY SIMILARITY.
 FT FT DISULFID; 72; 78.
 BY SIMILARITY.
 FT FT CARBOHYD; 101; 111.
 BY SIMILARITY.
 FT FT N-LINKED (GLCNAC, . .) (POTENTIAL).
 FT FT CONFLICT; 4; 4.
 L -> R (IN REF. 2).
 FT FT CONFLICT; 110; 110.
 I -> V (IN REF. 2).
 FT FT CONFLICT; 171; 171.
 M -> L (IN REF. 2).
 FT FT CONFLICT; 201; 201.
 S -> R (IN REF. 2).
 SQ SEQUENCE; 208 AA; 23446 MW; EFC996C13E3230A0 CRC64;
 Best Local Similarity 9.6%; Score 96; DB 1; Length 208;
 Matches 50; Conservative 26; Mismatches 86; Indels 40; Gaps 8;
 Query Match 9.6%; Score 96; DB 1; Length 208;
 Best Local Similarity 24.8%; Pred. No. 0.046;
 Matches 40; Conservative 20; Mismatches 64; Indels 33; Gaps 8;

QY 6 AVMLLILIPWTAQGRAVPGGSSPAWTQCOQLSOKLTLAWSAHPLVGHM-----DL 56
 DB 13 AVSLGLLUVMTS-AFPDPGPGLGEDPKNDNTPSPRLLTPEKTBALIKHIVDKISAIRKEI 71
 QY 57 REGDE-----ETNDYVPHICQGDCPDQGLRDSNSQFLQRIOHGLIFYEKILG-- 105
 DB 72 CENDECNSKETLAENKLKPKMERKGDFQSGF -NQAICLIKTTAGLEYQTYLDFL 129
 QY 106 SDIFTGEPSLLPDSPVQLHASLIGLSQLQ-----PCHHAWTQQIPSLSOPW 156
 DB 130 QNEFFGN----QETMELQSSITRLQIQLKETAGLTTPATH--TDMLEKMQSSNEW 181
 QY 157 QRLLRFKILRLQAFAVAAR 178
 DB 182 VKNAKVIIILRSLENFLQFSLR 203

RESULT 4
 CSF3_SHEEP
 ID CSF3_SHEEP
 AC Q28746;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Granulocyte colony-stimulating factor (G-CSF).
 GN CSF3.
 OS Ovis aries (Sheep).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95102116; PubMed=7528579;
 RA O'Brien P.M., Seow H.F., Rothel J.S., Wood P.R.;
 RT "Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDNA.",
 RL DNA Seq. 4:339-342(1994).
 CC !- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES (BY SIMILARITY).
 CC !- SUBUNIT: MONOMER.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- PTM: O-GLYCOSYLATED.
 CC !- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

RESULT 5
 CSF3_CANFA
 STANDARD; PRT; 175 AA.
 ID CSF3_CANFA
 AC P33834;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Granulocyte colony-stimulating factor (G-CSF).
 GN CSF3.
 OS Canis familiaris (Dog).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Canidae; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-94076341; PubMed=7504736;
 RA Lovejoy B./, Cescio D./, Eisenberg D./,
 RT "Crystal structure of canine and bovine granulocyte-colony
 stimulating factor (G-CSF)."
 RL J. Mol. Biol. 234:645-653(1993).
 CC !- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES (BY SIMILARITY).
 CC !- SUBUNIT: MONOMER.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- PTM: O-GLYCOSYLATED.
 CC !- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

DR PDB; 1BGG; 31-OCT-93.

-1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC purposes requires a license agreement (See <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch.

CC DR EMBL; BAA13118_1; - .

CC DR HSSP; P05231; IL6.

CC DR InterPro; IPR003573; IL6_MGF_GCSF.

CC DR InterPro; IPR003574; Interleukin_6.

CC DR Pfam; PF00489; IL6.

CC DR PRINTS; PR000433; IL6GCSFMGF.

CC DR PRODOM; PD000433; IL6GCSFMGF.

CC DR PRODOM; PD0004356; Interleukin_6; 1.

CC DR SMART; SM00126; IL6; 1.

CC DR SMART; SM00128; IL6; 1.

CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.

CC DR CYTOKINE; Glycoprotein; Growth factor; Signal.

CC KW BY SIMILARITY.

CC FT SIGNAL; 1 29

CC FT CHAIN; 30 208

CC FT DISULFID; 72 78

CC FT DISULFID; 101 111

CC FT CARBOHYD; 38 38

CC SO N-LINKED (GLCNAC. . .). (POTENTIAL).

CC SEQUENCE 208 AA; 23423 MW; E92E0BFBF3E230A0 CRC64;

Query Match 8.9%; Score 89; DB 1; Length 208;
Best Local Similarity 24.1%; Pred. No. 0.21; Gaps 7;
Matches 48; Conservative 27; Mismatches 90; Indels 34;

Query Match 8.9%; Score 89.5; DB 1; Length 175;
Best Local Similarity 24.7%; Pred. No. 0.16; Gaps 8;
Matches 40; Conservative 21; Mismatches 68; Indels 33; Gaps 8;

QY 6 AVMLLILPWTAGRAVGGSSPAWTOQQQLSOKLCILWAHSAPLYGHM-----DL 56

Db 13 AVSIGLLIWMTS-AFPITGPPLGDFKDNTPSRLLTTPTEALIKHIVDKISALARKEI 71

QY 57 REEGDE-----ETTNVDPHIQCQGDQGLRDNQSFCQLRHQGLLFYEKLIGK-- 105

Db 72 CERNDECNSKEELAENKKLKPMEERDGCFSGF--NOAICLKTAGGLEQYIQLDFL 129

QY 106 SDITTGEP-SLLPDSPVAQHLASLGLSQLQP-----GHHWETOQIPSUSPSPQWRL 159

Db 130 QNEFEQN----QETVMELOQSSIRTLLQIKEKTAGLITPTNTDMLEKQSSNEWVKN 184

QY 160 LLREKILRSLENFLQFSLR 178

Db 185 AKVIIILRSLENFLQFSLR 203

RESULT 6

Q28191 [1] IL6_CAPHI STANDARD; PRT; 208 AA.
Q28191 [2] 01-NOV-1997 (Rel. 35, Created)
Q28191 [3] 01-NOV-1997 (Rel. 35, Last sequence update)
Q28191 [4] 15-JUN-2002 (Rel. 41, Last annotation update)
Q28191 [5] Interleukin-6 precursor (IL-6).
Q28191 [6] IL6.
Q28191 [7] Capra hircus (Goat).
Q28191 [8] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Q28191 [9] Mammalia; Caprinae; Capra.
Q28191 [10] NCBI_TaxID=9325;
Q28191 [11] SEQUENCE FROM N.A.
Q28191 [12] MEDLINE=97392351; PubMed=9250586;
Q28191 [13] TAKAKURA H., MORI Y., TATSUJI M.; Molecular cloning of caprine IL-6 cDNA and its expression in insect cells.".
Q28191 [14] Arch. Allergy Immunol. 113:409-416(1997).
Q28191 [15] "FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
Q28191 [16] "SUBCELLULAR LOCATION: secreted.

RESULT 7

Q28193 [1] CSF3_HUMAN STANDARD; PRT; 207 AA.
Q28193 [2] ID CSF3_HUMAN
Q28193 [3] AC P09519;
Q28193 [4] DT 01-MAR-1989 (Rel. 10, Created)
Q28193 [5] DT 01-MAR-1989 (Rel. 10, Last sequence update)
Q28193 [6] DT 15-JUN-2002 (Rel. 41, Last annotation update)
Q28193 [7] DE Granulocyte colony stimulating factor precursor (G-CSF) (Pluripoietin) (Filigrastim) (Lenograstim).
Q28193 [8] DE OC Homo sapiens (Human).
Q28193 [9] OS Homo sapiens (Human).
Q28193 [10] OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Q28193 [11] NCBI_TaxID=9606;
Q28193 [12] RN [1]
Q28193 [13] RP SEQUENCE FROM N.A.
Q28193 [14] RX MEDLINE=96118679; PubMed=3484805;
Q28193 [15] RA Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O., Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
Q28193 [16] RT "Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor."
Q28193 [17] RN [2]
Q28193 [18] RP SEQUENCE FROM N.A.
Q28193 [19] RX MEDLINE=16220137; PubMed=243327.

RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
 RA Oheda M., Nomura H., Yamazaki T.;
 RT "The chromosomal gene structure and two mRNAs for human granulocyte
 colony-stimulating factor.";
 RT RL EMBO J. 5:575-581(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87116936; PubMed-3494901;
 RA Devlin J.J., Devlin P.E., Myanbo K., Lilly M.B., Rado T.A.,
 RA Warren M.K.;
 RT "Expression of granulocyte colony-stimulating factor by human cell
 lines.";
 RT JL Leukoc. Biol. 41:302-306(1987).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
 RA Rieder M.-J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 19-207 FROM N.A.
 RX MEDLINE-8611684; PubMed-2420009;
 RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,
 RA Murdoch D.C., Chain V.R., Bruszevski J., Tu H., Chen K.K.,
 RA Barrendt J., Platzer B., Moore A.S., Mertelsmann R., Welte K.;
 RT "Recombinant human granulocyte colony-stimulating factor: effects on
 RT normal and leukemic myeloid cells.";
 RL Science 232:61-66(1986).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE
 RX MEDLINE-93291942; PubMed-71685769;
 RA Clouston C.L., Hu S., Boone T.C., Lu H.S.;
 RT "Glycosidase digestion, electrophoresis and chromatographic analysis
 RT of recombinant human granulocyte colony-stimulating factor glycoforms
 RT produced in Chinese hamster ovary cells.";
 RL J. Chromatogr. A 637:55-62(1993).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE-91106200; PubMed-1281794;
 RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
 RT "Secondary structure of human granulocyte colony-stimulating factor
 RT derived from NMR spectroscopy.";
 RL FEBS Lett. 314:435-439(1992).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE-94304859; PubMed-7518249;
 RA Zink T., Ross A., Luers K., Clesiar C., Rudolph R., Holak T.A.;
 RT "Structure and dynamics of the human granulocyte colony-stimulating
 RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
 bundle protein.";
 RL Biochemistry 33:8453-8463(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-3281718; PubMed-7685117;
 RA Hill C.P., Osslund T.D., Eisenberg D.;
 RT "The structure of granulocyte-colony-stimulating factor and its
 RT relationship to other growth factors";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).
 CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY STIMULATING FACTORS ARE
 CYTOKINES THAT ACT IN HEMATOPOEISIS BY CONTROLLING THE PRODUCTION,
 DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS,
 OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES/MACROPHAGES. THIS
 CSF INDUCES GRANULOCYTES.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH CAN BE
 MODIFIED WITH UP TO TWO STATIC ACID RESIDUES (DONE IN
 RECOMBINANTLY EXPRESSED CSF FROM CHO CELLS).
 CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
 (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat
 neutropenia (a disorder characterized by an extremely low number
 of neutrophils in blood).
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -!- CAUTION: REF.4 MISQUOTES THE GENE NAME AS "CSF1".

CC -!- DATABASE: NAME=Neupogen/Granulokine;
 CC NOTE=Clinical information on Neupogen/Granulokine;
 CC WWW="http://www.neupogen.com/monograph/frame0.htm";
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC in the European Bioinformatics Institute. There are no restrictions on
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC DR EMBL; X03438; AAA27168.1;
 DR EMBL; M13008; AAA03056.1;
 DR EMBL; X03656; CAA27291.1;
 DR EMBL; X03655; CAA27290.1;
 DR EMBL; AF380025; AAC02469.1;
 DR EMBL; M17706; AAA355882.1;
 DR PIR; A24573; A24573;
 DR PIR; A25093; A25093;
 DR PDB; 1RHG; 31-TAN-94.
 DR PDB; 31-TUL-94.
 DR PRINTS; PR0433; IIGGCSFMGFG;
 DR PRODOM; PD008388; GCSF_MGF;
 DR SMART; SMO0126; LL6.1;
 DR PROSITE; PS0251; INTERLEUKIN_6.1.
 DR CYKINE; Growth factor; Glycoprotein; Signal; Alternative splicing;
 DR Polymorphism; Pharmaceutical; 3D-structure.
 DR SIGNAL 1 30
 FT CHAIN 31 30
 FT DISULFID 69 75
 FT DISULFID 97 107
 FT CARBOHID 166 166
 FT VARSPLIC 66 68
 FT VARIANT 157 157
 FT VARIANT 157 157
 FT VARIANT 174 174
 FT HELIX 41 65
 FT HELIX 69 71
 FT HELIX 77 86
 FT TURN 87 88
 FT HELIX 105 124
 FT TURN 125 127
 FT TURN 130 132
 FT HELIX 133 156
 FT TURN 157 158
 FT HELIX 176 203
 FT TURN 204 204
 SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;
 SQ
 Best Local Similarity 8.8%; Score 88.5%; DB 1; Length 207;
 Matches 51; Conservative 20; Mismatches 76; Indels 53; Gaps 12;
 QY 15 WTAQGRAPVGSSPANTQ----CQQ-----LSQKL---CLAWSAHP---LV 51
 Db 25 WTVQ-BATPLGPASSIPQSFLKCLEQVRKIQGDGAQEKLYSECATYKUCHPEELVLL 83
 QY 52 GMNDLREGDEETLWYHPIQCGDQPGQLRNSQFLQR-HQGLTFYENLGSDFITG 111
 Db 84 GH -----SLGPWPL-SSCPGSAQ-LAGCLSLQHSGLYQGL-QALEG 127
 QY 112 -EPSLILPDSPVAQHLASLGLSQLIQPEGHWWTOQPSLSPSO-----PWORLLR 162
 Db 128 ISPELGTPLDPLQDADFTATIOME---ELGMAPALQPTQGAMPFRASAFORRAGG 183
 QY 163 FKLRSQAFYAVAAVFYAH 182

Db	184	VLVASILQSFLEVSTRVLRH	203
RESULT 8			
CSF3_MOUSE	STANDARD;	PRT;	208 AA.
CDF_ID	CSF3_MOUSE	STANDARD;	PRT;
AC	P05920;		
DDT	01-MAR-1989 (Rel. 10, Created)		
DT	01-MAR-1989 (Rel. 10, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
GN	Granulocyte colony-stimulating factor precursor (G-CSF).		
OS	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;		
OX			
RESULT 9			
IL6_MOUSE	STANDARD;	PRT;	211 AA.
ID	IL6_MOUSE	STANDARD;	PRT;
AC	P08305;		
DDT	01-AUG-1988 (Rel. 08, Created)		
DT	01-AUG-1988 (Rel. 08, Last sequence update)		
DT	15-JUN-2003 (Rel. 41, Last annotation update)		
DE	Interleukin-6 precursor (IL-6) (Interleukin HP-1) (B-cell hybridoma growth factor).		
DE	IL6 OR IL-6.		
GN	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;		
OX			
RN	[1]	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RP	MEDLINE-87017003; PubMed=3489940;		
RX	TSUCHIYA M., ASANO S., KAZIRO Y., NAGATA S.; "Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor." Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).		
RN	[2]	SEQUENCE FROM N.A.	
RP	TSUCHIYA M., KAZIRO Y., NAGATA S.; "The chromosomal gene structure for murine granulocyte colony-stimulating factor." Eur. J. Biochem. 165:7-12(1987).		
CC	-1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCUTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCUTES.		
CC	-1- SUBUNIT: MONOMER.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- PTM: O-GLYCOSYLATED (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).		
DR	EMBL; M13926; AAA37672.1; -.		
DR	EMBL; X05402; CAA28986.1; -.		
DR	PIR; A29536; A29536.		
DR	PIR; A26496; A26496.		
DR	HSSP_P0919; 1RHG.		
DR	MGI; MGI:1339751; Cf3.		
DR	InterPro; IPR003629; GCSF_MGF.		
DR	InterPro; IPR003575; IL6_MGF_GCSF.		
DR	Pfam; PF00489; IL6_1.		
DR	PRINTS; PR00433; IL6_GCSFMGF.		
DR	PRODOM; P000388; GCSF_MGF; 1.		
DR	SMART; SMART00126; IL6; 1.		
DR	PROSITE; PS00254; INTERLEUKIN 6; 1.		
KW	Cytokine; Growth factor; Glycoprotein; Signal.		
FT	SIGNAL	1	30
FT	CHAIN	31	208
FT	DISULFID	72	78
FT	DISULFID	100	110
FT	CARBONYD	169	169
FT	SEQUENCE	208 AA;	22421 MW;
Query Match		8.7%	Score 87.5%; DB 1; Length 208;
Best Local Similarity		25.0%	Fred No. 29; Indels 41; Gaps 10;
Matches		23	Mismatches 59;
Conservative		41;	Gaps

- FT HELIX 65 69
FT TURN 70 71
FT HELIX 72 75
FT TURN 76 76
FT HELIX 83 85
FT TURN 87 89
FT HELIX 92 112
FT TURN 113 115
FT HELIX 118 120
FT HELIX 121 145
FT HELIX 164 191
FT TURN 192 192
SQ SEQUENCE 195 AA: 21431 MW: 8C06119E4ADFBAT3 CRC64;
- Query Match 8.0%; Score 80.5%; DB 1; Length 195;
Best Local Similarity 23.4%; Pred. No. 1.2;
Matches 48; Conservative 25; Mismatches 79; Indels 53; Gaps 11;
- Qy 7 VMLLILPPWTAQ---GRAVPGGSSPANTQ---C-----QQLSQKLCTLAWS 46
Db 3 LMLVQLLWISALWLVHETPLGKFLKCLEQWRKIQADGEIQLERCAAHKL 62
Qy 47 AHP---LYGHMDLREEGDEETNDVPHIQCGDGPQLRDNQFCQLQRHGLIFYEK 102
Db 63 CHPEEMLLRH-----SLGIPQAFL-SSCQSQQSLQLTS--CLNQLHGLEFLYQG 108
Qy 103 LIGSDIFTC-EPSLLPDSPVPAQLHASLGLSQLQEGHHWETQPLSPO----- 154
Db 109 LL--QALAGTISPELAFTDLTQLDVTFATNIWLQME---DGAAPAVQPTOGAMPTFT 162
Qy 155 -PWQRLLRFKILRSQAFYAVAAR 178
Db 163 SAFORRAGGYVIVASQHRFELAYR 187
- RESULT 11
ID FRZ3_DROME STANDARD; PRT; 581 AA.
AC 077438; Q917Z7; Q9N10; Q9u902; Q9w5D5;
DT 15-JUN-2002 (Rel. 41; Created)
DT 15-JUN-2002 (Rel. 41; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Frizzled protein 3 precursor (Frizzled-3) (DFz3).
GN FZ3 OR EG3.6 OR CG16785.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila.
OX NCBI_TAXID=727;
- RN SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=99429803; Published=10498678;
RA Sato A.; Kojima T.; Uti-Tei K.; Miyata Y.; Saigo K.;
RT "Frizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
of wingless signaling in wingless hypomorphic mutants";
RL Development 126:4421-4430 (1999).
RN SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=20171076; Published=10704878;
RA Sivasankaran R.; Calleja M.; Morata G.; Basler K.;
RT "The Wingless target gene *Dfz3* encodes a new member of the Drosophila
Frizzled family";
RL Mech Dev. 91:427-431(2000).
RN SEQUENCE FROM N.A. (SHORT ISOFORM).
RC STRAIN=Oregon R;
RX MEDLINE=20196011; Published=10731137;
RA Benos P.V.; Gatt M.K.; Ashburner M.; Murphy L.; Harris D.;
RA Demalle J.; Cadiou E.; Borkova D.,
RA Dreano S.; Gloux S.; Leelaire V.; Mottier S.; Galibert F.;
RA Minana B.; Karatos F.C.; Louis C.; Siden-Kiamos I.;
RA Papagiannakis G.; Spanos L.; Cox S.; Madueno E.; de Pablo B.,
RA Modolell J.; Peter A.; Schoettler P.; Werner M.; Mourkioti F.,
- RA Beinert N.; Dove G.; Schaefer U.; Jaekle H.; Bucheton A.;
RA Callister D.M.; Campbell L.T.; Darjamitsou A.; Henderson N.S.;
RA McMillan P.J.; Salles C.; Tait E.A.; Valenti P.; Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
melanogaster";
RL Science 287:2220-2222(2000).
RN [4]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN=Berkeley;
RX MEDLINE=20196006; Published=10731132;
RA Adams M.D.; Ceuliniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Anatantides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.,
Georg R.A.; Lewis P.V.; Richards S.; Ashburner M.; Henderson S.N.,
RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers Y-H.C.; Blaize M.; Pfeiffer B.D.,
RA Brandon R.C.; Baxter F.G.; Heit G.; Nelson C.R.; Miklos G.L.G.,
RA Doyle S.; Miklos G.L.G.,
RA Abrial J.F.; Agbayani A.; An H.-J.; Andrews-Pflanckoch C.; Baldwin D.,
RA Bailew R.M.; Basu A.; Bayrendale J.; Bayraktaroglu L.; Beasley E.M.,
RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Bolshakov S.,
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstedt P.; Brottier P.,
RA Burkit K.C.; Busam D.A.; Butler H.; Cadieu E.; Chandra I.,
RA Burkit K.C.; Busam D.A.; Dahlke C.; Davies P.,
RA Cherry J.M.; Cawley S.; Dahlen T.J.; Davenport L.B.;
RA de Pablos B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.I.; Dietz S.M.,
RA Dodson K.; Douc L.E.; Downes M.; Dugan-Rocha S.; Dunn P.,
RA Durbin R.K.J.; Evangelista C.C.; Ferraz C.; Ferriera S.; Fleischmann W.,
RA Foster C.; Gabrielian A.E.; Gaig N.S.; Gelbart W.M.; Glasser K.,
RA Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.,
RA Harris N.L.; Harvey D.; Heiman T.J.; Hernández J.R.; Houck J.,
RA Hostin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ibegwam C.,
RA Jalali M.; Kalush F.; Karpen J.A.; Ketchum K.A.,
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulip D.; Lai Z.,
RA Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.,
RA Liu X.; Mattes B.; McIntosh M.P.; McLeod P.; McPherson D.,
RA Merkulov G.; Milashina N.V.; Mobarry C.; Morris J.; Mosherf A.,
RA Mount S.M.; Moy M.; Murphy L.; Muzyk D.M.; Nelson D.L.,
RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacieb J.M.,
RA Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puris M.G.,
RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen T.,
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.,
RA Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.,
RA Swirskas R.; Tector C.; Turner R.; Venter E.; Wang A.-H.; Wang X.,
RA Wang Z.-Y.; Wasserman D.A.; Weinstock G.M.; Weissenbach J.,
RA Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.,
RA Ye J.; Yeh R.-F.; Zaveri J.S.; Zhang G.; Zhao M.; Zheng L.,
RA Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.;
RT "The genome sequence of drosophila melanogaster.";
RL Science 287:2185-2195(2000).
- CC -!- FUNCTION: Receptor for wnt proteins. Most of frizzled receptors
are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway, as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-proteins. Required to coordinate
the cytoskeletons of epidermal cells to produce a parallel array
of cuticular hairs and bristles.
- CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here), and a
short form; are produced by alternative splicing;
CC -!- TISSUE SPECIFICITY: Wing, leg and eye imaginal discs. In embryos,
CC expressed is seen in brain, proventriculus, Malpighian tubules,
CC anal plate and visceral mesoderm of parasegment 8.
- CC -!- DEVELOPMENTAL STAGE: Expressed in embryos from stage 11 and in
CC larvae.
- CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By
similarity).
- CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
RECEPTORS.

-> SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AB018565; BAA8467.1; .
 EMBL; AF193242; AAF33250.1; .
 EMBL; AL031583; CAAJ0896.1; .
 EMBL; AE003418; AACF5547.1; .
 EMBL; AE003418; AACG2363.1; .
 FlyBase; FBgn0027343; fz3.
 InterPro; IPR000539; Frizzled.
 InterPro; IPR000024; FZ_domain.
 InterPro; IPR000832; GPCR_secretin.
 Pfam; PF01534; Frizzled; 2.
 Pfam; PF01592; Fz; 1.
 PRINTS; PRO0489; FRIZZLED.
 SMART; SM00063; FRI; 1.
 PROSITE; PS50038; FZ; 1.
 PROSITE; P50261; G_PROTEIN_RECEP_F2; 4; 1.
 Multigene family; Receptor; G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal; Alternative splicing.
 SIGNAL 19
 CHAIN 20
 PROTEIN 3.
 DOMAIN 20
 DOMAIN 237
 TRANSMEM 258
 DOMAIN 259
 TRANSMEM 270
 DOMAIN 271
 TRANSMEM 292
 DOMAIN 292
 TRANSMEM 342
 DOMAIN 343
 TRANSMEM 359
 DOMAIN 360
 DOMAIN 381
 TRANSMEM 393
 DOMAIN 394
 DOMAIN 414
 TRANSMEM 442
 DOMAIN 443
 TRANSMEM 443
 DOMAIN 464
 TRANSMEM 488
 DOMAIN 489
 DOMAIN 509
 TRANSMEM 509
 DOMAIN 510
 DOMAIN 510
 DOMAIN 156
 DOMAIN 35
 SITE 410
 CARBOHYD 403
 SITE 579
 VARSPLIC 581
 CARBOHYD 54
 VARSPLIC 1
 VARSPLIC 56
 CONFLICT 56
 CONFLICT 192
 CONFLICT 276
 CONFLICT 276
 CONFLICT 304
 CONFLICT 376
 SEQUENCE 581
 AA; 63251 MW; 07A8BBFF2A933F93 CRC64;

Query Match 8.0%; Score 80.5%; DB 1; Length 581;
 Best Local Similarity 26.4%; Pred No. 4.3; Mismatches 75; Indels 31; Gaps 9;
 Matches 46; Conservative 22; Mismatches 75; Indels 31; Gaps 9;

6 AVMLLILPW----TAQGRA----VPGSSPAPWTQCOOLSQLKLT---LAWSAHP-LVG 52
 4 ASLILHLTWAATIAANGAGHNGPVASSAGPNQCCOPIAVSACOGIGYNNNTALPNLAG 63

53 HMDLREGDEETTNQPHIQCGDCPDQLGRDNQS---CLQRHQGL---IFYKEKLGS 106
 64 HTN-QLEAELQIATKLYPLIESGCSRRAFLQCLSSLFPCTDPVRPAACKLCEVRYRE 122

107 DIFTGEPLLDPDSPVAQQLHAASLLGLSLOSSQPEGHWEHQ---QIPSLSPSQ 155

RESULT	12	CMEAPPLEM-----ELMPSFLNCDGLIPOKEKELCMQIPOEVAVPGSSPGP	179
MGF-CHICK			
ID	MGE CHICK	STANDARD:	PRT: 201 AA.
AC	PI13854;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Myelomonocytic growth factor precursor (MGF).		
OS	Gallus gallus (Chicken)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;		
OC	Gallus.		
NCBI_TaxID	9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89231616; PubMed=2785450;		
RA	Leutz A., Damm K., Sternberg E., Kowenz E., Ness S., Frank R.,		
RA	Gaussohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.,		
RT	"Molecular cloning of the chicken myelomonocytic growth factor reveals relationship to interleukin 6 and granulocyte colony stimulating factor."		
RT	EMBO J. 8:175-181(1989).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=92195319; PubMed=1549124;		
RA	Sternbeck E., Blattner C., Graf T., Leutz A.;		
RA	"Structure of the chicken myelomonocytic growth factor gene and specific activation of its promoter in avian myelomonocytic cells by protein kinases."		
RT	Mol. Cell. Biol. 12:1728-1735(1992).		
-!	FUNCTION: HEMATOPOIETIC GROWTH FACTOR THAT STIMULATES THE PROLIFERATION AND COLONY FORMATION OF NORMAL AND TRANSFORMED CELLS OF THE MYELOID LINEAGE.		
CC	-!- SUBCELLULAR LOCATION: Secreted.		
CC	-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a cooperation between the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is not modified and this statement is not removed. Usage by and for entities requires a license agreement (see http://www.isb-sib.ch or send an email to license@isb-sib.ch).		
CC	EMBL; M85034; AAA48594.1; -.		
DR	EMBL; X14477; CAA32639.1; -.		
DR	PIR; S03633; S03633.		
DR	PIR; A42241; A42247.		
DR	HSSP; P35834; 1BGD.		
DR	InterPro; IPR003629; GCSF_MGF.		
DR	InterPro; IPR003573; IL6_MGF_GCSF.		
DR	Pfam; PF00489; IL6; 1.		
DR	PRINTS; PR00433; IL6GCSFGMF.		
DR	ProDom; PDO00388; GCSF_MGF; 1.		
DR	SMART; SM00126; IL6_1.		
DR	PROSITE; PS00254; INTERLUKIN_6; 1.		
KW	Growth factor; Glycoprotein; Signal.		
FT	SIGNAL	1	23
FT	CHAIN	24	201
FT	DISULFID	61	67
FT	DISULFID	89	99
FT	CARBONYD	123	123
FT	CARBONYD	137	137
SQ	SEQUENCE	201 AA:	22373 MW;
SQ			24038DD21B424AE6 CRC64;
Query Match	7	7.9%	Score 79.5; DB 1; Length 201;
Best Local Similarity	28.6%	Pred. No. 1.6	
Matches	36;	Conservative	19; Mismatches 52; Indels 19;
OV	69	PHIOCGG-DCDPOGURDNSOFCORTHOGLIFYFKIGSDIFTGPSLIPDS-----P-	

RESULT 13
FAS_CHICK STANDARD; PRTR; 2511 AA.

ID FAS_CHICK
ID P12216;
AC P12216;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fatty acid synthase (EC 2.3.1.85) [Includes: EC 2.3.1.38; EC 2.3.1.39;
EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 3.1.2.14].
DE FASN OR FAS.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;

RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-11.
RN STRAN=White leghorn; TISSUE=Liver;
RN MEDLINE=95031085; PubMed=7944406;
RN RT "Amino-terminal blocking group and sequence of the animal fatty acid
synthase.";
RN RT SEQUENCE OF 75-1775 FROM N.A.
RN RT TISSUE=Liver;
RN MEDLINE=89382777; PubMed=2734291;
RN RT Holzer K.P., Liu W., Hammes G.G.;
RT "Molecular cloning and sequencing of chicken liver fatty acid
synthase cDNA";
RN Proc. Natl. Acad. Sci. U.S.A. 86:4387-4391(1989).
RN SEQUENCE OF 1568-2512 FROM N.A., AND PARTIAL SEQUENCE.
RN MEDLINE=89139436; PubMed=291973;
RN RA Yuan Z., Liu W., Hammes G.G.;
RN RT "Molecular cloning and sequencing of DNA complementary to chicken
liver fatty acid synthase mRNA.";
RN RT A novel cDNA extension procedure. Isolation of chicken fatty acid
synthase cDNA clones.";
RN RT J. Biol. Chem. 263:3750-3757(1988).
RN [4] SEQUENCE OF 1752-2512 FROM N.A.
RN RP SEQUENCE OF 2202-2512 FROM N.A.
RN MEDLINE=88320436; PubMed=2842766;
RN RX Yuan Z., Liu W., Hammes G.G.;
RN RT "Molecular cloning and sequencing of DNA complementary to chicken
liver fatty acid synthase mRNA.";
RN RT Proc. Natl. Acad. Sci. U.S.A. 85:6328-6331(1988).
RN [5] SEQUENCE OF 2202-2512 FROM N.A.
RN RP SEQUENCE OF 89088152; PubMed=3207710;
RN RX Kasturi R., Chirala S.S., Pazirandeh M., Wakil S.J.;
RN RA "Characterization of a genomic and cDNA clone coding for the
liver fatty acid synthase gene";
RN RT "Complete amino acid sequence of chicken liver acyl carrier protein
derived from the fatty acid synthase.";
RN RL Arch. Biochem. Biophys. 270:92-98(1989).

RN [7] SEQUENCE OF 2209-2508.
RN RP STRAN=White leghorn;
RN RC MEDLINE=89088151; PubMed=3207709;
RN RX Yang C.-Y., Huang W.-Y., Chirala S.S., Wakil S.J.;
RN RT "Complete amino acid sequence of the thioesterase domain of chicken
liver fatty acid synthase.";
RN RL Biochemistry 27:773-777(1988).
RN I81]
RN RP SEQUENCE OF 667-674 AND 1698-1709.
RN RA Chang S.-I., Hammes G.G.;
RN RT "Amino acid sequences of pyridoxal 5'-phosphate binding sites and
fluorescence resonance energy transfer in chicken liver fatty acid
synthase.";
RN RL Biochemistry 28:3781-3788(1989).
CC -!- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
CC THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATALYTIC ACTIVITIES AND AN
CC ACYL CARRIER PROTEIN.
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
CC long-chain fatty acid + (N+1) CoA + N CO(2) + 2N NADP(+).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + [acyl-carrier protein] = CoA +
CC acetyl-lacyl-carrier protein.
CC -!- CATALYTIC ACTIVITY: Malonyl-CoA + [acyl-carrier protein] = CoA +
CC malonyl-lacyl-carrier protein.
CC -!- CATALYTIC ACTIVITY: Acyl-lacyl-carrier protein + malonyl-lacyl-
carrier protein = 3'-oxoacyl-lacyl-carrier protein + CO(2) +
CC [acyl-carrier protein].
CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-lacyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-lacyl-carrier protein + NADPH.
CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxylalimoyl-lacyl-carrier protein]
CC = 2-hexadecenoyl-lacyl-carrier protein + H(2)O.
CC -!- CATALYTIC ACTIVITY: Acyl-lacyl-carrier protein + NADPH.
CC -!- 2,3-dihydroacyl-lacyl-carrier protein + NADPH.
CC -!- CATALYTIC ACTIVITY: Oleoyl-lacyl-carrier protein] + H(2)O = [acyl-
carrier protein] + oleate.
CC -!- SUBUNIT: HOMODIMER, WHICH IS ARRANGED IN A HEAD TO TAIL FASHION.
CC -!- CAUTION: REF 3 AND REF 5 SEQUENCES DIFFER FROM THAT SHOWN FROM
POSITION 2351 ONWARDS DUE TO A FRAMESHIFT.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; J04485; AAB46389; 1; -;
DR EMBL; J03860; AAA4876; 1; -;
DR EMBL; J02839; AAB82106; 1; ALT_SEQ.
DR PR; A33918; XYCIFA.
DR PR; A32015; A32015.
DR InterPro; IPR001227; Ac transferase.
DR InterPro; IPR002085; Adh_an_family.
DR InterPro; IPR000794; ketoacyl-synth.
DR InterPro; IPR003880; Epanine_attach.
DR InterPro; IPR001031; Thioesterase.
DR Pfam; PF00107; adh_zinc; 1.
DR Pfam; PF00109; ketoacyl-synth; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHINE; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR Pfam; PF00550; pp_binding; 1.
DR Pfam; PF00698; Acyl_transf; 1.
DR Pfam; PF00925; Thioesterase; 1.
DR Pfam; PF02801; ketoacyl-synth_C; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHINE; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR Pfam; PF00109; ketoacyl-synth; 1.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
KW Fatty acid biosynthes; Multifunctional enzyme; Phosphopantetheine;
KW Transferase; Hydrolase; Oxidoreductase; Lyase; NADP; Acetylation;
KW Alternative splicing; Pyridoxal phosphate.
FT INT_MET 0 0
FT DOMAIN 1 ?411 1 BETA-KETOACYL SYNTHASE.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TAXID=10090;

RN [1]

RP

RT

RT "A novel gene of the ADAMTS family predicts ADAMTS-10, a metalloprotease with unique structural features and expression pattern";

RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (BY similarity).

CC -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY SIMILARITY).

CC -!- DOMAIN: BELONGS TO PEPTIDASE FAMILY M12B.

CC -!- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. Long as its content is in no way modified this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL: AF302012; AAH97226; 1; -.

DR InterPro; IPR00884; TSP1.

DR SMART; SM00209; TSP1; 4.

DR PROSITE; PS5002; TSP1; 1.

KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Repeat;

KW Extracellular matrix.

FT NON_TER 1 1

FT DOMAIN <1 51

CYS-RICH.

FT DOMAIN 52 174

SPACER.

FT DOMAIN 171 232

TSP TYPE-1 1.

FT DOMAIN 234 290

TSP TYPE-1 2.

FT DOMAIN 294 348

TSP TYPE-1 3.

FT DOMAIN 353 399

TSP TYPE-1 4.

FT CARBOHYD 86 86

N-LINKED (GLCNAC . . .) (POTENTIAL).

FT CARBOHYD 141 141

N-LINKED (GLCNAC . . .) (POTENTIAL).

FT CARBOHYD 238 238

N-LINKED (GLCNAC . . .) (POTENTIAL).

SQ SEQUENCE 450 AA: 48861 MW: 2377D0E2CFBFDFCA CRC64;

Query Match 7.8%; Score 78.5; DB 1; Length 450;
 Best Local Similarity 24.2%; Pred. No. 5;
 Matches 36; Conservative 13; Mismatches 69; Indels 31; Gaps 6;

Qy 14 PWTAGRRAVPGGSSPAWTOCQLSORKLTAWSAHPLYGHMDLRREGDDETTNDVP--- 69
 Db 179 PWTKCSAQCAQGGSQVQVCCR--NQLDSSAVAPVHYCGSHSKLPKRORACNTEPCPDPWV 235

Qy 70 ---HIQCGGGCDPQGLRDNSQFCLOTRHOGLIFYKLGGSDITFGEPSLIPDSVAQLHA 126
 Db 236 VGNWSRSRSCD-AGYRSRSVVCQRVS-----AAEEKAIDDASACPQPRP 279

Qy 127 SLLGLSQ -LIQPEGHWWETQQIPSLSPS 153
 Db 280 PYLEACQGPMPPE --WATLDWSECTPS 305

Search completed: November 20, 2002, 11:53:24
 Job time : 9.8545 secs

GenCore version 5.1.3
 Copyright (c) 1993 - 2002 Compugen Ltd.

4 protein - protein search, using sw model
 run on: November 20, 2002, 11:51:20 ; Search time 26.0182 Seconds
 (without alignments)
 1496.75 Million cell updates/sec

title: US-09-658-699-2
perfect score: 1004
sequence: 1 MIGSRAYMLLILPWTQGR.....QAFVAVARVFAHGAATLSP 189

scoring table: BLOSUM62
Gapop 10.0 , **Gapext** 0.5

searched: 671580 seqs, 206047115 residues

total number of hits satisfying chosen parameters: 671580

minimum DB seq length: 0
maximum DB seq length: 200000000

post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

SPREMBL 21:

database :

SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID
1	1004	100.0	189	4	Q9H2A5
2	1000	99.6	189	4	Q9NPF7
3	846	84.3	193	6	Q9N2H9
4	784.5	78.1	196	11	Q91ZB4
5	718.5	71.1	196	11	Q9EQ14
6	97	9.7	195	6	Q9GJ00
7	86	8.6	1121	16	Q9PG80
8	85.5	8.5	352	15	Q9PZ44
9	85.5	8.5	363	4	Q9NRZ4
10	84.5	8.3	210	11	Q9WVQ8
11	83	8.3	137	15	Q9PZ45
12	82	8.2	208	6	Q9XTB0
13	81.5	8.2	858	11	Q923K0
14	81.5	8.1	212	11	Q912L3
15	81.5	8.1	540	5	Q95K25
16	80.5	8.0	232	16	Q96557

ALIGNMENTS						
RESULT	1					
Q9H2A5		PRELIMINARY;				
Q9H2A5;						
AC		PRM;	189 AA.			
DT	01-MAR-2001	(TREMBLrel.	16,	Created)		
DT	01-MAR-2001	(TREMBLrel.	16,	sequence update)		
DT	01-DIC-2001	(TREMBLrel.	19,	Last annotation update)		
DE	Interleukin 23	p19 subunit.				
Homo sapiens (Human)						
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
NCBI_TaxID=9606;						
LN	[1]					
RN		SEQUENCE FROM N.A.				
RP		SEQUENCE_ID=10322; PubMed=11114383;				
RX		MEDLINE=200567322;				
RA	Oppermann, B.	Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F., Yu N., Wang J., Singla K., Zonin F., Vaishberg E., Churakova T., Liu M.-R., Gossman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S., Moore K.W., Rennick D., de Waal Malefyt R., Hannum C., Bazan J.F., Kastlein R. A.				
RA	"Novel p19 Protein Engages IL-12p40 to Form a Cytokine, IL-23," with Biological Activities Similar as Well as Distinct from IL-12.";					
RL	Immunity 13:715-725(2000).					
DR	EMBL; AF301620; AAC37222.1; -					
DR	InterPro; IPR03573; IIG6_MGE_GCSF.					
SMAR	SM00126; 116; 1					
SEQUENCE	189 AA;	20744 MW;	BFB5C0F42D4C1E3A CRC64;			
Query	Match	100.0%	Score 1004;	DB 4;	Length 189;	
	Best Local Similarity	100.0%	Pred. No. 7	2-96;		
Matches	189;	Conservative	Mismatches 0;	Indels 0;	Gaps 0	
Qy	1	MLGSRAVMILLILIPWTAQGRAYPGGSSPAWTCQQLSQKLCTLAWSAHPLYGHMDLREG	60			
Ds	1	MLGSRAVMILLILIPWTAQGRAYPGGSSPAWTCQQLSQKLCTLAWSAHPLYGHMDLREG	60			
Qy	61	DEETTNDYPHIQCQDGCDPQLRDNSOFCLORHQGLFYERKLGSDPFTGPSPSLPDSP	120			
Ds	61	DEETTNDYPHIQCQDGCDPQLRDNSOFCLORHQGLFYERKLGSDPFTGPSPSLPDSP	120			
	57	DEETTNDYPHIQCQDGCDPQLRDNSOFCLORHQGLFYERKLGSDPFTGPSPSLPDSP	120			

QY	121	VAQHSLIGLSQLQPEGHHWETQQTIPSLSPSQWPQRLLRFKILRSQAFVAVARVF	180
Db	121	VAQHSLIGLSQLQPEGHHWETQQTIPSLSPSQWPQRLLRFKILRSQAFVAVARVF	180
QY	181	AHGATLSP 189	
Db	181	AHGATLSP 189	
RESULT 2			
Q9NPF7			
ID	Q9NPF7	PRELIMINARY;	
AC	Q9NPF7;	PRT;	189 AA.
DT	01-OCT-2000	(TREMBREL 15, Created)	
DT	01-OCT-2000	(TREMBREL 15, Last sequence update)	
DT	01-JUN-2001	(TREMBREL 17, Last annotation update)	
DE	SGRF precursor.		
GN	Homo sapiens (Human).		
OS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID	9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=SPLEEN;		
RA	Hirata Y., Kosuge Y.;		
RT	"SGRF: a novel member of the IL-6/G-CSF family";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB30000; BA93666.1; -.		
DR	EMBL; AB30001; BA93667.1; -.		
DR	InterPro:IPR003573; IL6_MGF_GCSF.		
DR	SMART; SMD0126; IL6; 1.		
DR	SMART; SMD0126; IL6; 1.		
KW			
FT	SIGNAL	1	19
FT	CHAIN	20	189
FT	SEQUENCE	189 AA;	20730 MW;
SQ			SGRF.
			POTENTIAL.
Query Match	99.6%	Score 1000;	DB 4;
Best Local Similarity	99.5%	Pred. No. 1.9e-95;	Length 189;
Matches	188;	Conservative 0;	Mismatches 1;
		Indels 0;	Gaps
QY	1	MIGSRAYMLLIPWTAGRAYPGSSPAWTQCGQSOKLCTLAWSAHPLYGHMDLREG	60
Db	1	MIGSRAYMLLIPWTAGRAYPGSSPAWTQCGQSOKLCTLAWSAHPLYGHMDLREG	60
QY	61	DEETNDYPHIQCGDGPQGLRDNSOCLQRTHQGLIFYEKLLSDIFTEPSLLPDSP	120
Db	61	DEETNDYPHIQCGDGPQGLRDNSOCLQRTHQGLIFYEKLLSDIFTEPSLLPDSP	120
QY	121	VAQHSLIGLSQLQPEGHHWETQQTIPSLSPSQWPQRLLRFKILRSQAFVAVARVF	180
Db	121	VGQHSLIGLSQLQPEGHHWETQQTIPSLSPSQWPQRLLRFKILRSQAFVAVARVF	180
Qy	181	AHGATLSP 189	
Db	181	AHGATLSP 189	
RESULT 3			
Q9NZH9			
ID	Q9NZH9	PRELIMINARY;	
AC	Q9NZH9;	PRT;	193 AA.
DT	01-OCT-2000	(TREMBREL 15, Created)	
DT	01-OCT-2000	(TREMBREL 15, Last sequence update)	
DT	01-JUN-2001	(TREMBREL 17, Last annotation update)	
DE	SGRF.		
GN	Os scrofa (pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
NCBI_TaxID	9823;		
	[1]		

Q9EQ14	PRELIMINARY;	PRT;	196 AA.
ID Q9EQ14;			
AC Q9EQ14;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DT 23 p19 subunit (Interleukin 23, alpha subunit p19).			
GN IL23A.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20567322; PubMed=11114383;			
RA Oppermann, B., Lesley, R., Blom, B., Timans, J.C., Xu, Y., Hunte, B., Vega, F.,			
RA Yu, N., Wang, J., Singh, K., Zonin, F., Vaiberg, E., Churakova, T.,			
RA Liu, M.-R., Gorman, D., Wagner, J., Zurawski, S., Liu, Y.-J., Abrams, J.S.,			
RA Moore, K.W., Rennick, D., de Waal, Malefyt, R., Hannum, C., Bazan, J.F.,			
RA Kastlein, R.A.;			
RT Novel p19 Protein Engages IL-12p40 to Form a Cytokine, IL-12. ";			
RT Biological Activities Similar as Well as Distinct from IL-12. "			
RL Immunity 13:715-725(2000).			
RN [2]			
RP SEQUENCE FROM N.A.			
RA Strasberg, R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
RL EMBL; AF301619; ANG37231.1; -;			
DR BC019953; AAH19933.1; -;			
DR MGII: MGI:1932410; II123a.			
DR InterPro; IPRO03573; IL6_MGF_GCSF.			
DR SMART; SM00126; IL6; 1.			
SQ SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;			
Query Match 71.68; Score 718.5; DB 11; Length 196;			
Best Local Similarity 74.6%; Pred. No. 2.5e-66;			
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;			
QY 1 MLGSSAVMLLLLPWTAQGRAVPGGSSPANTQCQQLSQQKLCTLAWSAHPLVGHMD-LREE 59			
Db 1 MLDGRAVINMLWLPLWWTGGLAPRSSLQPRSLRNCLMILAWNAHAPAGIMNLRE 60			
QY 60 GDEENTNDYPHIQCGDQGCDPQGLRDNSQQCLOTHIYKLGDSIFTGPSLIPDS 119			
Db 61 EDEETKNNPRIODGEDCPQGLKDQNQFCLOTRIQLAFYKHLDSDFKGEPALLDS 120			
QY 120 PVAOLHASLGLGSQLOPEGHHWETOIPSLSQSPQWORLRLRFKILRSLQQFAYAARV 179			
Db 121 PMEQLHTSLLGLSQQLQEDHPRETOOMPSLSQWQRPLRSKILRSLQQFLAIARY 180			
QY 180 FAHGAAATLS 188			
Db 181 FAHGAAATLT 189			
RESULT 6			
Q9GJU0	PRELIMINARY;	PRT;	195 AA.
ID Q9GJU0;			
AC Q9GJU0;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
GN G-CSF.			
OS Balaustis catus (Cat).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX NCBI_TaxID=9655;			
RP SEQUENCE FROM N.A.			
RA Yamamoto, A., Iwata, A., Tuchiya, K., Katsumata, A., Oishi, K.,			
RA Tsujimoto, H., Hasegawa, A., Ueda, S.,			
RT Molecular cloning and expression of the cDNA encoding feline			

Machado M.A.,	Madeira A.M.B.N.,	Madeira H.M.F.,	Marino C.L.,	WQOCDTQTLRKRFITFCSTAWPOVPLQGGTETWLPEGSINYNIILQDLCRERGKWEV	67
Marques M.V.,	Martins E.A.L.,	Martins B.M.F.,	Matsuoka A.Y.,	DB	8
Menck C.F.M.,	Miracca E.C.,	Miyaki C.Y.,	Monteiro-Vitorello C.B.,	QY	69
Nencini D.H.,	Nagai M.A.,	Nascimento A.L.T.O.	Netto L.E.S.,	DB	68
Nhani A.P. Jr.,	Nobreira F.G.,	Nunes L.R.,	Oliveira M.A.,	PyYQTF --- -ESLRUNSOGL	109
de Oliveira M.C.,	de Oliveira R.C.,	Palmieri D.A.,	Paris A.,	PHIQCGDGDQGLRDNSQLQLRQIHQGLFYKEKLGSDFDIFTGEPLIP- --- -DSPYAQ	123
Peixoto B.R.,	Pereira G.A.C.,	Pereira H.A.Jr.,	Pesquero J.B.,	1 :	1 :
Quaggio R.B.,	Roberto P.G.,	Rodrigues V.,	de Rosa A.J.M.,	1 :	1 :
de Rosa V.E. Jr.,	de Sa R.G.,	Santelli R.V.,	Sawasaki H.E.,	1 :	1 :
da Silva A.C.R.,	da Silva A.M.,	Santos J.R.,	Vettore A.L.,	1 :	1 :
da Silveira J.F.,	Silvestri M.L.Z.,	Siqueira W.J.,	de Souza A.A.,	1 :	1 :
de Souza A.P.,	Terenzi M.F.,	Truffi D.,	Ishihiko M.H.,	1 :	1 :
de Souza H.,	Van Sluys M.A.,	Verjovkova-Almeida S.,	Vettore A.L.,	1 :	1 :
Zago M.A.,	Zatz M.,	Neidans J.,	Setubal J.C.,	1 :	1 :
Complete Proteome,	PS00215; MITOCH_CARRIER;	UNKNOWN_1.			
SEQUENCE 1121 AA;	124406 MW;	581EDA1B12EA5318	CRC64;	RESULT 9	
Query Match 8.68;	Score 86;	DB 16;	Length 1121;	Q9NRZ4	PRELIMINARY;
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	ID Q9NRZ4;	PRT;
Matches 41; Conservative 18;	Mismatches 23;			AC Q9NRZ4;	363 AA.
SEQUENCE FROM N.A.				DT 01-OCT-2000 (TREMBLrel. 15, Created)	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
Matches 41; Conservative 18;	Mismatches 23;			DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
SEQUENCE FROM N.A.				DE Gag.	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	DE GAG.	
Matches 41; Conservative 18;	Mismatches 23;			GN GAG.	
SEQUENCE FROM N.A.				OS Homo sapiens (Human).	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Matches 41; Conservative 18;	Mismatches 23;			OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	
SEQUENCE FROM N.A.				NCBI_TaxID=9606;	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	RN [1]	
Matches 41; Conservative 18;	Mismatches 23;			RP SEQUENCE FROM N.A.	
SEQUENCE FROM N.A.				RX MEDLINE=202B4713; PubMed=10826480;	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	RA Voisset C., Bouton O., Bedin F., Duret L., Mandrand B., Mallet F.,	
Matches 41; Conservative 18;	Mismatches 23;			RA Parhomas Bacallao G.	
SEQUENCE FROM N.A.				RA "Chromosomal distribution and coding capacity of the human endogenous retrovirus HEV-W family".	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	RT RTAIDS Res. Hum. Retroviruses 16:731-740 (2000).	
Matches 41; Conservative 18;	Mismatches 23;			RT AF156961; AAFT4213.1; -.	
SEQUENCE FROM N.A.				DR InterPro; IPR00840; Gag_MA.	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	DR InterPro; IPR003036; Gag_p30.	
Matches 41; Conservative 18;	Mismatches 23;			DR Pfam; PF01140; Gag_MA; 1.	
SEQUENCE FROM N.A.				DR Pfam; PF02093; Gag_p30; 1.	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	SQ SEQUENCE 363 AA; MW: C65A4BD4A73785AB CRC64;	
Matches 41; Conservative 18;	Mismatches 23;			Query Match 8.58%; Score 85.5; DB 4; Length 363;	
SEQUENCE FROM N.A.				Best Local Similarity 24.6%; Pred. No. 1.4;	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	Matches 45; Conservative 13; Mismatches 50; Indels 75; Gaps 10;	
Matches 41; Conservative 18;	Mismatches 23;			QY 19 GRAVPGGSSPA----WIFQ---QQLSOK---LCTLAWSAHPLVGHMDLREGD---- 61	
SEQUENCE FROM N.A.				Db 2 GNIPPKAKTFLRCILLENWQCDQFDQLTRRKRFICSTAWPOYPLQGTWPEGSINYNN 61	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	QY 62 ----EETTQGLDRNNSQFQCLQRHQLFYKEKLGSDFDIFTG 111	
Matches 41; Conservative 18;	Mismatches 23;			Db 62 ILQDLFCKREGKWSVEPVYQVTF----PSLRLNSQLC----KKCGL-OPT 103	
SEQUENCE FROM N.A.				QY 112 EPSLLP----DSPAQLHASLQLSQLQPE----GHHWETOQIPSLS 151	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	Db 104 SPQSPPPVSPVPPTPSSNKDPP----LTCVQKEIDKGVNNEPKSANPRC 153	
Matches 41; Conservative 18;	Mismatches 23;			RESULT 10	
SEQUENCE FROM N.A.				Q9WVQ8 PRELIMINARY;	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	AC Q9WVQ8	
Matches 41; Conservative 18;	Mismatches 23;			DB 01-NOV-1999 (TREMBLrel. 12, Created)	
SEQUENCE FROM N.A.				DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)	
Matches 41; Conservative 18;	Mismatches 23;			DE IL-6 (Fragment).	
SEQUENCE FROM N.A.				OS Mesocricetus auratus (Golden hamster).	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Matches 41; Conservative 18;	Mismatches 23;			OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gricetinae;	
SEQUENCE FROM N.A.				OC Mesocricetus.	
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;	NCBI_TaxID=1036;	
Matches 41; Conservative 18;	Mismatches 23;			OX	
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		
Matches 41; Conservative 18;	Mismatches 23;				
SEQUENCE FROM N.A.					
Best Local Similarity 23.78%;	Pred. No. 4.7;	Indels 58;	Gaps 9;		

RESULT 12											
[1]	RN	SEQUENCE FROM N.A.									
RP	STRAIN=APA; TISSUE=KIDNEY;										
RC	Nishida E.;										
RA	"APA hamsters IL-6 partial cDNA."										
RT	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.										
EMBL	AB028355; BAA78766..1;										
DR	HSSP; P05231; 1AU;										
InterPro; IPR03573; IL6_MGF_GCSF;											
InterPro; IPR03574; Interleukin_6.											
PFam; PF00489; IL6..1;											
PRINTS; PD00433; IL6GSPRMF;											
SMART; SM00126; IL6..1;											
PROSITE; PS00254; INTERLEUKIN_6..1;											
NON_TER	1	210 AA:	24060 MW:	BD9319AFBB913AB3	CRC64;						
SEQUENCE											
Query Match	8.48;	Score 84.5;	DB 11;	Length 210;							
Best Local Similarity	24.70;	Pred. No. 0.93;									
Matches	44;	Conservative	24;	Mismatches	69;	Indels	41;	Gaps	8;		
Qy	28	PANTQCQ-----LSQRKLTLAWSAHPLYGHMDLREGD-----ETTNNDVPH 70									
Db	42	PVTTTSQVGGLVTVYLREIVELRKLC----NNNP---QCMD----NDYVLENNLEIPV 91									
Qy	71	IQCGDGCDPOGLRDNSQFLCQRIHQGLIFYERKLGSIDFTGEPSLLPDSPVAOLHASLLG 130									
Db	92	IQINDGCLQTYK---NWEICLKLITSGELDYQIYL--EFVNNVNODNKKDKARYTQSTIKT 147									
Qy	131	LSOULLQPEGHMNETQIIPS-----LSPSQPWQRILLRFKLRLSQAFAYAAR 178									
Db	148	LSOIFQEVKGPDKIVTPSPSKATIMKLESQKEMPRTKTIKLKALDEELEVTRMR 205									
RESULT 11											
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus-like particles."										
RT	virology 260:1-9(1999);										
RL	EMBL; AF123880; AAD48374..1; -.										
KW	multiple sclerosis (fragment).										
OS	polyprotein.										
OC	Viruses; Retroviridae.										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RX	MEDLINE=9333590; Published=10405350;										
RA	Komurian-Pradel F., Parainos-Baccala G., Bedin F., Ouranian-Paraz A.,										
RA	Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,										
RA	Perron H.;										
RT	"Molecular cloning and characterization of MSRV-related sequences associated with retrovirus										

DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.
 DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
 KW RECEPTOR.
 SQ SEQUENCE 858 AA; 94530 MW; 686A7E52426798A CRC64;
 Query Match 8.2%; Score 82; DB 11; Length 858;
 Best Local Similarity 27.4%; Pred. No. 8..9;
 Matches 51; Conservative 10; Mismatches 65; Indels 60; Gaps 11;
 Qy 3 GSRAVMLLILPWTQAGRAVPGSSPAWTQCCQLSOKLTCAWAHPVLGIMDLRREGDE 62
 Db 570 GEPVVLSSLI-----LCLVGLALAAGLSVH----HW----- 599
 Qy 63 ETTNDVPHIQCGCDPQGLRDNSOFCQLRIHQGLIFYERKLGSIDTGFEDP---SLLPDS 119
 Db 600 ---DSDPVQASEG-----SQFCGLICLGFLPSVLI---FPGRSSASCLAQQ 642
 Qy 120 PVAQHASILG-LSQLQPEGHHWETQIQPSLSPSPWQRLRFLRKTLRSQAFYAAAR 178
 Db 643 PMA--HLPTGCLSTLFLQAAETFVESELP-LS---WANWLCSY--LRLGIAWLVLSA 693
 Qy 179 VFAHGA 184
 Db 694 TFVEAA 699

RESULT 14

Q912L3 PRELIMINARY; PRT; 212 AA.
 ID Q912L3
 AC 0912L3;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DR AF421389 AAL18819.1;
 DR IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR IPR003580; Protachykinin.
 DR Pfam: PF00489; IL6_1.
 DR Prodom; PD00436; Interleukin_6; 1.
 DR SMART; SM00203; TK_1.
 DR PROSITE; PS00924; INTERLEUKIN_6; UNKNOWN_1.
 SQ SEQUENCE 212 AA; 24406 MW; 97E1C47ED080D5D CRC64;

Query Match 8.1%; Score 81..5; DB 11; Length 212;
 Best Local Similarity 23.8%; Pred. No. 1..9;
 Matches 38; Conservative 25; Mismatches 64; Indels 33; Gaps 7;

Qy 35 QLSQKLTLMASAHPLVGHMDLREEGD--EFTTDVPHIQCGDCDPQGL-RDNSOFLQ 91
 Db 65 QMSKELCN-----NNPDCMTHDDALENNIDLPPVFERNDCCFQTQYDREN--CIL 112
 Qy 92 RIHQGLIFYE--KLIGQDFITGPESLPLPPSPVAOLHASLIGLSQLLOPGEHHWETQIP 148
 Db 113 KITSGLDQYILEFLKNNQDNK----KERVATQNSTKALNQILKOEVKDFGKTATP 167
 Qy 149 S-----LSPSOPWQRLLRFKTLRSQAFYAAAR 178
 Db 159 SPTSKVLLMELLESQRDWPTKTIQILKALEEFKIKMR 207

RESULT 15

SUMMARIES									
Result No.	Score	Query	Match	Length	DB	ID	Description		
1	1004	100.0	189	20	AYY9783		Human interleukin-1	FT	Peptide
2	1004	100.0	189	20	AAW5002		Human interleukin-1	FT	Protein
3	1004	100.0	189	21	AAB01981		Human interleukin-1	FT	Protein
4	1004	100.0	189	22	AAB7120		Human IL-B30. Homologous protein.	XX	
5	1000	99.6	189	21	AYV94966		Human secreted protein	PP	
6	1000	99.6	189	21	AAY4606		SGRF Protein sequence	XX	
7	1000	99.6	189	22	ABU2287		Human PRG5798 polypeptide	PR	
8	1000	99.6	189	22	AAB8070		Human extracellular matrix protein	PR	
9	718.5	71.6	196	20	AYY9784		Mouse interleukin-1	XX	
10	718.5	71.6	196	20	AAW5003		Mouse interleukin-1	PA	

•	Gencore version 5.1.3	Murine interleukin-1	1.1	718.5	71.6	196	21	AB01982	
	Copyright (c) 1993 - 2002 CompuGen Ltd.	Murine IL-B30. Mu	1.2	718.5	71.6	196	22	AA347121	
		Partial pig interleukin-1	1.3	463	46.1	102	20	AYZ9787	
		Pig interleukin-B3	1.4	463	46.1	102	20	AAW5004	
		Mature porcine interleukin-1	1.5	463	46.1	102	21	AAB01983	
		Granulopoietic act	1.6	107	10.7	175	21	AAB15206	
		Granulopoietic act	1.7	105	10.5	175	21	AAB15207	
		Granulopoietic act	1.8	103	10.3	175	21	AAB15202	
		Human granulocyte	1.9	103	10.3	175	21	ABJ5207	
		Human G-CSF analog	2.0	102	10.2	174	21	ABJ4859	
		Granulopoietic act	2.1	102	10.2	174	23	AAE14695	
		IL-3 containing fu	2.2	102	10.2	175	21	ABJ4856	
		IL-3 containing fu	2.3	102	10.2	175	16	AAR79298	
		IL-3 containing fu	2.4	102	10.2	175	16	AAR79299	
		Myelopoietin (MPO)	2.5	102	10.2	175	16	AAR79311	
		Myelopoietin (MPO)	2.6	102	10.2	175	16	AAE13973	
		Human interleukin-1	2.7	102	10.2	175	16	AAE13979	
		Human interleukin-1	2.8	102	10.2	175	21	AAV33180	
		Human interleukin-1	2.9	102	10.2	175	21	AAV53192	
		Human interleukin-1	3.0	102	10.2	175	21	AAE1393	
		Myelopoietin (MPO)	3.1	102	10.2	175	22	AAE13932	
		Myelopoietin (MPO)	3.2	102	10.2	175	22	AAE13975	
		Myelopoietin (MPO)	3.3	102	10.2	175	22	AAE13986	
		Myelopoietin (MPO)	3.4	102	10.2	175	22	AAE13987	
		Myelopoietin (MPO)	3.5	102	10.2	175	22	AAE14029	
		Myelopoietin (MPO)	3.6	102	10.2	175	22	AAE14032	
		Myelopoietin (MPO)	3.7	102	10.2	175	22	AAE14038	
		Myelopoietin (MPO)	3.8	102	10.2	175	22	AAE14041	
		Myelopoietin (MPO)	3.9	102	10.2	175	22	AAE14044	
		Myelopoietin (MPO)	4.0	102	10.2	175	22	AAE14047	
		Myelopoietin (MPO)	4.1	102	10.2	175	22	AAE14050	
		Myelopoietin (MPO)	4.2	102	10.2	175	22	AAE14053	
		Myelopoietin (MPO)	4.3	102	10.2	175	22	AAE14056	
		Myelopoietin (MPO)	4.4	102	10.2	175	22	AAE14059	
		Human sapiens.	45	102	10.2	175	22		
		Location/Qualifiers	XX						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DRS1; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Homo sapiens.						
		XX	OS						
		XX	Key						
		FT	Peptide						
		FT	Protein						
		XX	IL-B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						
		FT	Protein						
		XX	IL-3						
		XX	B30						
		XX	DNAX						
		XX	cytokine receptor						
		XX	interleukin B30; DRS1; IL-B30						
		XX	soluble receptor subunit 1						
		XX	inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.						
		XX	Human sapiens.						
		XX	Location/Qualifiers						
		Key	XX						
		FT	Peptide						

XX Kastlein RA, Mattson JD, McClanahan TK;
 PI XX WPI; 1999-527306/44.
 DR N-PSBB; AAZ08065.
 XX PT New receptor subunits useful in the treatment inflammatory disorders
 XX PS Claim 2; Page 26-27; 133pp; English.
 XX CC The present invention describes a composition (I) comprising DNA X
 CC cytochrome receptor subunit I (DCRS1) protein and DNAX soluble receptor
 CC subunit I (DSR1) protein, which together encode a new mammalian
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
 CC proteins, or DRS1 and IL-B30, proteins. (I) comprising DRS1 and DCRS1
 CC is useful for screening for ligands (i.e. agonists/antagonists) from
 CC a library of compounds, which are useful for modulating the physiology
 CC or development of a cell or tissue culture e.g. inflammatory responses,
 CC innate immunity and/or morphogenic development. (R) ant bodies and
 CC ligands are useful for treatment of conditions, especially immunological
 CC disorders, associated with conditions exhibiting abnormal expression of
 CC (R). (R) is useful as a phosphatase labeling enzyme to label substrates,
 CC and the subunits DRS1 and DRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and
 CC variants from other individuals or species. The present sequence
 CC represents the specifically claimed human IL-B30, for use in the
 XX composition of the present invention.
 XX Sequence 189 AA:
 Query Match 100 0%; Score 1004; DB 20; Length 189;
 Best Local Similarity 100.0%; Pred. No. 3.2e-97; Mismatches 0; Indels 0; Gaps 0;
 Matches 189; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 MLGRRAVMLLLPMTAQGAVAPGGSSPAWTOCQQLSQKLTLAWSAHPLVGHMDLREG 60
 Db 1 MLGRRAVMLLLPMTAQGAVAPGGSSPAWTOCQQLSQKLTLAWSAHPLVGHMDLREG 60
 Qy 61 DEETINDVPHIQCGDQCDPLGRNSQCLQRHQLFKEKLGSDFTGEPSLLPDSP 120
 Db 61 DEETINDVPHIQCGDQCDPLGRNSQCLQRHQLFKEKLGSDFTGEPSLLPDSP 120
 Qy 121 VAQLHSLGLSQLLQPEGHWTQIPSPSOPWQLLRFKTLRSQLAFAVAAVRF 180
 Db 121 VAQLHSLGLSQLLQPEGHWTQIPSPSOPWQLLRFKTLRSQLAFAVAAVRF 180
 Qy 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 XX AC AAW95002;
 XX DT 21-MAY-1999 (first entry)
 XX DE Human interleukin-B30 (IL-B30) polypeptide.
 XX KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
 KW inflammatory condition; drug screening; human.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..21
 FT Peptide /note= "signal peptide"
 FT Protein 22..189
 FT /note= "mature protein"
 PN WO9905280-A1.
 XX PD 04-FEB-1999.
 XX PF 24-JUL-1998; 98WO-US15423.
 XX PR 25-JUL-1997; 97US-0900905.
 XX PA (SCHIE) SCHERRING CORP.
 XX PI Bazan JF;
 XX DR 1999-142935/12.
 DR N-PSDB; AAX17786.
 XX PT Newly isolated or recombinant polynucleotide encoding mammalian
 CC cytokine interleukin B30 (IL-B30), including fragments - useful for
 PT regulating activation, development, differentiation and function of
 PT various cell types, and for diagnosing and treating conditions
 PT associated with IL-B30.
 XX
 Claim 2; Page 8-9; 83pp; English.
 XX This represents a human cytokine interleukin-B30 (IL-B30) polypeptide.
 CC Host cells containing a vector comprising the IL-B30 nucleic acid are
 CC used for recombinant production of the protein. The polynucleotides
 CC are useful for diagnosis of IL-B30 mediated conditions, and forensic
 CC science (e.g. to distinguish rodent from human, or as a marker to
 CC distinguish between different cells exhibiting differential expression or
 CC modification patterns). The IL-B30 (including fragments), together with
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They
 CC are also used for treating conditions associated with abnormal physiology
 CC or development, including inflammatory conditions. The polypeptide
 CC cytokine should mediate cytokine synthesis and proliferation in cells.
 CC 100 0%; Score 1004; DB 20; Length 189;
 CC Best Local Similarity 100.0%; Pred. No. 3.2e-97;
 CC Mismatches 0; Indels 0; Gaps 0;
 CC Matches 189; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 MLGRRAVMLLLPMTAQGAVAPGGSSPAWTOCQQLSQKLTLAWSAHPLVGHMDLREG 60
 Db 1 MLGRRAVMLLLPMTAQGAVAPGGSSPAWTOCQQLSQKLTLAWSAHPLVGHMDLREG 60
 Qy 61 DEETINDVPHIQCGDQCDPLGRNSQCLQRHQLFKEKLGSDFTGEPSLLPDSP 120
 Db 61 DEETINDVPHIQCGDQCDPLGRNSQCLQRHQLFKEKLGSDFTGEPSLLPDSP 120
 Qy 121 VAQLHSLGLSQLLQPEGHWTQIPSPSOPWQLLRFKTLRSQLAFAVAAVRF 180
 Db 121 VAQLHSLGLSQLLQPEGHWTQIPSPSOPWQLLRFKTLRSQLAFAVAAVRF 180
 Qy 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 XX AC AAB01981;
 XX DT 27-SEP-2000 (first entry)
 XX ID AAB01981 standard; Protein; 189 AA.
 XX AC AAB01981;
 XX DE Human interleukin-B30 (IL-B30).
 XX KW Interleukin-B30; IL-B30; human; cytokine; cellular signalling;
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
 KW granulocyte colony stimulating factor; immune disorder;

KW inflammatory disease; autoimmune disease; antigen; antibody.
 XX OS Homo sapiens
 XX FH Location/Qualifiers
 Key Peptide 1..21
 /note= "Signal peptide"
 FT Protein 22..189
 /note= "Mature human IL-B30"
 FT XX 04-JUN-2001 (first entry)
 XX Human IL-B30.
 PN US6060284-A.
 DE Human IL-B30.
 XX KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;
 ID AAB47120 standard; protein; 189 AA.
 XX KW INNgamma; Th1 response; autoimmune disease; chronic inflammation;
 AC AAB47120;
 XX KW memory T-cell; leucocyte; rheumatoid arthritis; osteoarthritis;
 KW memory T-cell; leucocyte; rheumatoid arthritis; osteoarthritis;
 KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;
 KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;
 KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;
 KW Castleman's disease.
 PI XX Homo sapiens.
 DE Homo sapiens.
 XX Location/Qualifiers
 DR 09-MAY-2000.
 PD 24-JUL-1998; 98US-0122443.
 XX 25-JUL-1997; 97US-0053765.
 PR (SCHE) SCHERRING CORP.
 PA XX
 PA Batzler JF;
 PI XX
 XX WPI: 2000-364420/31.
 DR N-PSDB; AAA53577.
 XX Novel recombinant DNA encoding cytokines especially interleukin-B30
 PT useful as probes or primers for diagnosing immune disorders including
 PT autoimmune or chronic inflammatory conditions -
 PR XX
 PS Claim 1; Column 5-8; 32PP; English.
 XX This sequence represents human interleukin-B30 (IL-B30). IL-B30
 CC is a novel cytokine, exhibiting significant homology to IL-6 and
 CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical
 CC role in signalling between immune or other cells during an immune
 CC response. The precise role if IL-B30 is not yet known - it is likely to
 CC have either a stimulatory or an inhibitory effect on haematopoietic cells
 CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.
 CC Alternatively, it may affect vascular physiology or development, or have
 CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and
 CC antagonists are useful in the diagnosis and treatment of disorders
 CC associated with abnormal expression or activity of IL-B30 e.g.,
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are
 CC useful for recombinant expression of IL-B30 in a host cell, and as a
 CC source of probes and primers. The IL-B30 probes and primers can be used
 CC to detect levels of IL-B30 expression or autoimmune disorder. IL-B30 nucleotides may
 CC also be used to identify homologous genes in other species. IL-B30
 CC protein or its fragments are useful as antigens for raising antibodies to
 CC various linear and conformational epitopes. Such antibodies may be used
 CC to detect levels of IL-B30 protein in a sample.
 XX Sequence 189 AA:
 SQ Query Match 100.0%; Score 1004; DB 21; Length 189;
 Best Local Similarity 100.0%; Pred. No. 3.e-97;
 Matches 189; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 MLGSRAYMLLPLPWTQGRAVPGGGSPATWQCOQLSOKLTLMASAHPLVGMDLREG 60
 1 MLGSRAYMLLPLPWTQGRAVPGGGSPATWQCOQLSOKLTLMASAHPLVGMDLREG 60
 QY 61 DEETNDYPHIQCGDGPGLRDNSOFLORIQLIFVKEKLGSDFITGEPSLLPDSP 120
 Db 61 DEETNDYPHIQCGDGPGLRDNSOFLORIQLIFVKEKLGSDFITGEPSLLPDSP 120
 QY 121 VAQIHLASLGSLQQLQPFHMETQIPLSLSQPKWRLRERKTLRSQAFVAARWF 180
 Db 121 VAQIHLASLGSLQQLQPFHMETQIPLSLSQPKWRLRERKTLRSQAFVAARWF 180
 QY 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189

CC	IL-12 p40/IL-B30 is useful as an immunogen for the production a	PT	New polynucleotides encoding secreted proteins, which may have e.g.
CC	antiseria or antibodies specific for binding.	PT	nutritional, chemokine, immune stimulating or suppressing,
XX		PT	hematopoiesis regulating, tissue growth, activation/inhibition
SQ	Sequence 189 AA;	PT	antiinflammatory or tumor inhibition activity -
		XX	
Query Match	100.0% Score 1004; DB 22; Length 189;	PS	Claim 147; Page 597; 641 pp; English.
Best Local Similarity	100.0% Pred. No. 3.2e-9; Mismatches 0; Indels 0; Gaps 0;	XX	AAA16618 to AAA16697 encode the human secreted proteins given in
Matches	189; Conservative 0;	CC	CC ANY94980 to AA16698 isolated from human adult brain, adult thyroid,
Qy	1 MLGSRAVMLLLPLWTAQGRAVPGCCSSPAWTQCGQLSOKLCTLAWSAHPVHMDLREG 60	CC	CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,
Db	1 MLGSRAVMLLLPLWTAQGRAVPGCCSSPAWTQCGQLSOKLCTLAWSAHPVHMDLREG 60	CC	CC adult placenta, adult testis, whole embryo, adult cartilage, kidney,
Qy	61 DEETINNDVPHIOCCSDGCDPGLRDNNSQFLQRTHQGLIFYEKULGSDIFTGEPSLIPDSP 120	CC	CC foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,
Db	61 DEETINNDVPHIOCCSDGCDPGLRDNNSQFLQRTHQGLIFYEKULGSDIFTGEPSLIPDSP 120	CC	CC and adult bladder, cDNA libraries. The polynucleotides and proteins are
Qy	121 VAQHASLGLSQLIOPQEHHWETQPISSLSPSOPWRLLRFKLRSLQAFAVAAARVF 180	CC	CC predicted to have biological activities which would make them suitable
Db	121 VAQHASLGLSQLIOPQEHHWETQPISSLSPSOPWRLLRFKLRSLQAFAVAAARVF 180	CC	CC for treating, preventing or ameliorating medical conditions in humans
Qy	181 AHAATLSP 189	CC	CC and animals. The polynucleotides can be used as markers for tissues in
Db	181 AHAATLSP 189	CC	CC which the protein is preferentially expressed, as molecular weight
RESULT 5	AAY94966 standard; Protein; 189 AA.	CC	CC markers on Southern gels, and as chromosome markers or tags to identify
ID	AAY94966	CC	CC chromosomes or to map gene positions. The proteins can be used in the
ID	AAY94966 standard; Protein; 189 AA.	CC	CC treatment of immune deficiencies and disorders, such as severe combined
AC	AAY94966;	CC	CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
XX		CC	CC infections. These infections include human immunodeficiency virus (HIV),
SQ	Sequence 189 AA;	CC	CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
DT	16 JUN-2000 (first entry)	CC	CC candidiasis. The proteins can be used to treat autoimmune disorders such
DE	Human secreted protein clone rk80_3 protein sequence SEQ ID NO:138.	CC	CC as connective tissue disease, multiple sclerosis, systemic lupus
XX		CC	CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
KW	Human; secreted protein; immunostimulant; immunosuppressant; virucide;	CC	CC Guillain-Barré syndrome, autoimmune thyroiditis, insulin dependent
KW	KW antidiabetic; antifungal; cytostatic; antiinflammatory; dermatological;	CC	CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
KW	KW antiasthmatic; antiarthritic; antirheumatic; protozoicide;	CC	CC autoimmune inflammatory eye disease. The proteins can also be used to
KW	KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;	CC	CC treat allergic conditions, such as asthma. AAY16698 to AAA16774 represent
KW	KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;	CC	CC probes for the human secreted proteins from the present invention.
KW	KW connective tissue disease; multiple sclerosis; erythema nodosum;	XX	XX
KW	KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;	XX	XX
KW	KW Guillain-Barré syndrome; autoimmune thyroiditis; myasthenia gravis;	XX	XX
KW	KW insulin dependent diabetes mellitus; graft-versus-host-disease;	XX	XX
KW	KW autoimmune inflammatory eye disease; allergy	XX	XX
OS	Homo sapiens.	XX	XX
XX	WO200009552-A1.	XX	XX
PN	24-FEB-2000.	XX	XX
PD	XX	XX	XX
PF	13-AUG-1999;	XX	XX
XX	99WO-US18298.	XX	XX
PR	14 AUG-1998;	98US-0096622.	RESULT 6
PR	17-AUG-1998;	98US-0096615.	AAY54606
PR	14-SEP-1998;	98US-0099229.	ID
PR	23-OCT-1998;	98US-0105368.	XX
PR	08-JAN-1999;	99US-0115234.	AC
PR	12-FEB-1999;	99US-011931.	XX
PR	18-FEB-1999;	99US-0120575.	DT
PR	30-APR-1999;	99US-0132020.	01-FEB-2000 (first entry)
PR	11-AUG-1999;	99US-0096622.	XX
XX		DE	SGRF protein sequence.
PA	(GENE) GENETICS INST INC.	XX	XX
XX	Jacobs K, McCoy JM, Lavallie ER, Steininger RJ, Spaulding V;	KW	SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
PI	Merberg D, Treacy M, Agostino MJ,	XX	KW immune system; haematopoietic system; therapy.
PI	Wong GG, Clark RF, Fechtel K;	XX	OS Homo sapiens.
XX		XX	PN WO954357-A1.
DR	2000-205979/18.	XX	28-OCT-1999.
XX		PD	

XX PR 02-DEC-1999; 99WO-US28564.
 XX PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30995.
 PR 30-DEC-1999; 99WO-US31243.
 PI PR 06-JAN-2000; 2000WO-US00277.
 XX PR 06-JAN-2000; 2000WO-US00376.
 DR PR 11-FEB-2000; 2000WO-US03565.
 DR PR 18-FEB-2000; 2000WO-US04341.
 PT PR 18-FEB-2000; 2000WO-US04414.
 PT PR 24-FEB-2000; 2000WO-US04914.
 PT PR 24-FEB-2000; 2000WO-US05004.
 PT PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 CC PR 21-MAR-2000; 2000WO-US07532.
 CC PR 30-MAR-2000; 2000WO-US08439.
 CC PR 17-MAY-2000; 2000WO-US13705.
 CC PR 22-MAY-2000; 2000WO-US14042.
 CC PR 30-MAY-2000; 2000WO-US14341.
 CC PR 02-JUN-2000; 2000WO-US15244.
 CC PR 10-NOV-2000; 2000WO-US30873.
 SQ Sequence 189 AA;
 Query Match 99.6%; Score 1000; DB 21; Length 189;
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;
 Matches 188; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
 PS
 XX
 PT Novel cytokine-like protein, with activity of supporting proliferation
 PT of myeloid cells, useful in treating abnormality of cell proliferation
 PT in immune and haematopoiesis systems -
 XX
 PS Claim 1; Fig 1; 69pp; Japanese.
 XX
 CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
 CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
 CC family. The protein can be used in drugs for treating diseases due to
 CC abnormality of cell proliferation in the immune system and haematopoietic
 CC system.
 XX
 PS Sequence 189 AA;
 Query Match 99.6%; Score 1000; DB 21; Length 189;
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;
 Matches 188; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
 QY 1 MIGSRAYMLLLPWTNQGRAPVGSSPAWCQQLSOKLCTLAWSAHPLYGHMDIREEG 60
 Db 1 MIGSRAYMLLLPWTNQGRAPVGSSPAWCQQLSOKLCTLAWSAHPLYGHMDIREEG 60
 QY 61 DEETNDVPHQCGDGDQGLRDNQSFCQRLHQGLIFYEKULGSDFTGEPSSLPDSP 120
 Db 61 DEETTNVPHQCGDGDQGLRDNQSFCQRLHQGLIFYEKULGSDFTGEPSSLPDSP 120
 QY 121 VAQLHASLGLSQLQDEGHHWETQIPLSTLSPSQWPQRILLREFKIRSLQAVAVARYF 180
 Db 121 VQQLHASSLGLSQLQPEGHHWETQIPLSTLSPSQWPQRILLREFKIRSLQAVAVARYF 180
 QY 181 AHGAATLSP 189
 QY 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 RESULT 7
 ID AU12287 standard; Protein; 189 AA.
 AC AU12287;
 XX DT 24-OCT-2001 (first entry)
 XX DE Human PRO5798 polypeptide sequence.
 XX KW Human secretory and transmembrane; PRO: mammalian: cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX OS Homo sapiens.
 XX PN W0200140466-A2.
 XX PD 07-JUN-2001.
 XX PF 01-DEC-2000; 2000WO-US32678.
 XX PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 09-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 30-DEC-1999; 99WO-US30995.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14341.
 PR 02-JUN-2000; 2000WO-US15244.
 PR 10-NOV-2000; 2000WO-US30873.
 XX PA (GENETH) GENENTECH INC.
 XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tunas D, Watanabe CR, Wood WI, Zhang Z;
 XX DR N-PSDB; ASSEG 1359.
 XX PR 2001-408281/43.
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect other
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical or liver tumours by comparing PRO
 PT polyptide expression in cell sample to that in a control sample.
 XX DR N-PSDB; ASSEG 1359.
 PS Claim 12; Fig 232; 813pp; English.
 XX AAU12172-AU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polyptide expression in cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation of
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear tricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (BDMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX SQ Sequence 189 AA;
 Query Match 99.6%; Score 1000; DB 22; Length 189;
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;
 Matches 188; Conservative 0; Mismatches -1; Indels 0; Gaps 0;
 Qy 1 MIGSRAYMLLLPWTNQGRAPVGSSPAWCQQLSOKLCTLAWSAHPLYGHMDIREEG 60
 Db 1 MIGSRAYMLLLPWTNQGRAPVGSSPAWCQQLSOKLCTLAWSAHPLYGHMDIREEG 60
 Qy 61 DEETTDNDVPHQCGDGDQGLRDNQSFCQRLHQGLIFYEKULGSDFTGEPSSLPDSP 120

Db	61 DEETNDVPHIQCQDGCFQURDNSQFCFLQRHOGIIFYKLLGSDFLGEPSLIPDPSP	CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists, CC agonists, pharmaceutical compositions, and antibodies may also be used CC for treating or preventing disorders associated with increased or CC decreased expression or activity of EXCS. EXCS polynucleotides may also CC be used to detect and quantify gene expression in biopsied tissues in which expression of EXCS may be correlated with the disease, to determine CC presence or excess expression of EXCS, to monitor regulation of EXCS CC levels during therapeutic intervention, to detect the presence of CC associated disorders as targets in microarray to generate hybridization CC probes, and to detect differences in gene sequences among normal, carrier CC or affected individuals. Antibodies may also be used in diagnosing CC disorders, in monitoring patients being treated with EXCS agonists, CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS CC of the invention.
XX	XX	XX Sequence 189 AA;
AC	AAB48070; standard; protein; 189 AA.	SQ
XX	XX	Query Match 99.6%; Score 1000; DB 22; Length 189;
DT	19-MAR-2001 (first entry)	Best Local Similarity 99.5%; Pred. No. 8.5e-97;
XX	DE Human extracellular signaling molecule (EXCS) (ID 2933038CD1).	Mismatches 0; Gaps 0;
XX	Extracellular signaling molecule; EXCS; anti-inflammatory; human;	Matches 188; Conservative 0;
KW	immunosuppressive; cytotoxic; neuroprotective; gastrointestinal;	Indels 0;
KW	viricide; antibacterial; anti-HIV; human immunodeficiency virus;	Gaps 0;
KW	antinflammatory; cerebroprotective; nootropic; antiviral; antifungal;	
KW	anticonvulsant; tranquilizer; neuroleptic; vasoconstrictor; gynecological;	
KW	keratolytic; protozoacide; gene therapy.	
OS	Homo sapiens.	
XX	XX	RESULT 9
PN	WO2000070049-A2.	AAV29784
PD	23-NOV-2000.	ID AAV29784 standard; Protein: 196 AA.
XX	XX	XX
PF	19-MAY-2000; 2000WO-US13975.	AC AAV29784;
XX	XX	XX
PR	19-MAY-1999; 99US-0134949.	DT 04-NOV-1999 (first entry)
PR	15-JUL-1999; 99US-0144270.	DE Mouse interleukin B30.
PR	30-JUL-1999; 99US-0157508.	XX
PR	04-OCT-1999; 99US-0157508.	KW DNA soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
XX	XX	KW Interleukin B30; DRS1; IL-B30; cytokine receptor; innate immunity;
PA	(INCYT) INCYTE GENOMICS INC.	KW inflammatory disorder; inflammatory response; innate immunity;
XX	PI Tang YT, Yue H, Lai P, Burford N, Bandman O, Baughn MR;	KW morphogenetic development; immunological disorder.
PI	Zhang Y, Lu DAM, Patterson C,	XX
XX	WPI: 2001-025021/03.	OS Mus sp.
DR	N-PSDB: AAC843006.	XX
XX	New human extracellular signaling nucleic acids and polypeptides useful	Key
PT	for diagnosing, treating and preventing infections and	Location/Qualifiers
PT	gastrointestinal, neurological, reproductive, and	Peptide
PT	autoimmune/inflammatory disorders	Signal
XX	Claim 1: Page 92: 114pp; English.	Protein
PS	CC The invention provides human extracellular signaling molecules (EXCS)	FT /label= IL-B30
XX	CC and polynucleotides which identify and encode EXCS. EXCS can be	FT 22..196
CC	expressed by standard recombinant methodology. The amino acid and nucleic	FT WO940195-A1.
CC	acid sequences of EXCS are useful for diagnosing, treating and	XX
CC	preventing infections and gastrointestinal (peptic ulcer, dysphagia,	PN
CC	pancreatitis), neurological (e.g., epilepsy, ischemic cerebrovascular	XX
CC	disease, stroke), reproductive (infertility, ovulatory defects,	PD 12-AUG-1999.
CC	endometriosis), autoimmune (actinic keratosis, acquired	XX
CC	immunodeficiency syndrome (AIDS), Addison's disease), and cell	PF 05-FEB-1999; 99WO-US02600.
CC	proliferative disorders including cancers (of the breast, adrenal gland,	XX
CC	bone); they may also be used to treat fatal familial insomnia,	PR 13-MAY-1998; 98US-0078194.
CC	nutritional and metabolic diseases of the nervous system, myopathies,	PR 06-FEB-1998; 98US-0073941.
CC	mental disorders (anxiety, schizophrenia, mood, as well as infections	PA (SCHE) SCHERING CORP
CC	caused by parasites (malaria, leishmania, trypanosoma), viral	XX
CC	(adenovirus, coronavirus, flavivirus), bacterial (e.g., pneumococcus,	PI Kastelein RA, Mattson JD, McClanahan TK;
CC	staphylococcus, bacillus), and fungal (aspergillus, blastomycoses,	

XX WPI: 1999-527306/44.
DR N-PSDB; AAB08866.

XX New receptor subunits useful in the treatment inflammatory disorders

PS Claim 2; Page 27-28; 133pp; English.

XX The present invention describes a composition (I) comprising DNA X
CC cytokine receptor subunit I (DCRS1) protein and DNA X soluble receptor
CC subunit I (DSRS1) protein, which together encode a new mammalian
CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
CC proteins, or DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1
CC is useful for screening for ligands (i.e. agonists/antagonists) from
CC a library of compounds, which are useful for modulating the physiology
CC or development of a cell or tissue culture e.g. inflammatory responses,
CC innate immunity and/or morphogenic development. (R), antibodies and
CC ligands are useful for treatment of conditions, especially immunological
CC disorders, associated with conditions exhibiting abnormal expression of
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,
CC and the subunits DRS1 and DCRS1 are useful as immunogens for generating
CC antibodies, or as antigens for binding antibodies. Nucleic acids
CC encoding (R) are useful for identifying related DNAs and mRNAs, and
CC variants from other individuals or species. The present sequence
CC represents the specifically claimed mouse IL-B30, for use in the
CC composition of the present invention.

XX Sequence 196 AA;

Query Match Score 718.5; DB 20; Length 196;
Best Local Similarity 74.6%; Pred. No. 3.2e-67;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MIGSRAVMLLILLPPTAQRAVPGSSAWTCQQLSQKLTCLANSAAHPLVGHMD-LREE 59
Db 1 MLDCAVIMLWLLPWTQGLAVPRSSSDWAOCQQLSRNLCMANAHAPAGHMMLRE 60

QY 60 GDEETNDVPHIQCGDGPQGLRDNSQFCQLRQHQLTYEKLGSDFITGEPSPLLPS 119
Db 61 EDEETNINVRIPQCDGCPQGLKDNSQFCQLRQHQLTYEKLGSDFITGEPALLPS 120

QY 120 PVAQIHLASLGLSQLQPEGHMWTQIPSLSPQMPQLLRFKTLRSLOAFVAVAARY 179
Db 121 PMEQIHLTSLLGLSQLQPEDHPRTQMPSLSSQQQRPLRSKTLRSLOAFIAARY 180

QY 180 FAHGAATLS 188
Db 181 FAHGAATLF 189

RESULT 10
AAB01982 standard; Protein; 196 AA.

XX Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
KW inflammatory condition; drug screening; mouse.

XX DT 21-MAY-1999 (first entry)

DE Mouse interleukin-B30 (IL-B30) polypeptide.

XX AC AAB01982;

XX OS Mus sp.

XX PH Key Location/Qualifiers
FT Peptide 1..21 "signal peptide"
FT Protein 22..196 "/note= "mature protein"
FT PN W09905280-A1.

XX XX PD 04-FEB-1999.
XX PE 24-JUL-1998; 98WO-US15423.
XX PR 25-JUL-1997; 97US-0900905.
XX PA (SCHE) SCHERTING CORP.
XX PI Bazar JF;
XX DR WPI; 1999-142935/12.
XX DR N-PSDB; AAX17787.

XX PT Newly isolated or recombinant polynucleotide encoding mammalian
PT cytokine interleukin-B30 (IL-B30), including fragments - useful for
PT regulating activation, development, differentiation and function of
PT various cell types, and for diagnosing and treating conditions
PT associated with IL-B30

XX PS Claim 2; Page 9-10; 83pp; English.

XX This represents a mouse cytokine interleukin-B30 (IL-B30) polypeptide.
CC host cells containing a vector comprising the IL-B30 nucleic acid are
CC used for the recombinant production of the protein. The polynucleotides
CC are useful for diagnosis of IL-B30 mediated conditions, and forensic
CC science (e.g. to distinguish rodent from human, or as a marker to
CC distinguish between different cells exhibiting differential expression or
CC modification patterns). The IL-B30 (including fragments), together with
CC antibodies that bind to IL-B30 are useful for teaching purposes. They
CC are also used for treating conditions associated with abnormal physiology
CC or development, including inflammatory conditions. The polypeptide
CC cytokine should mediate cytokine synthesis and proliferation in cells.
CC IL-B30 is useful for drug screening to identify compounds having binding
CC affinity to IL-B30.

XX SQ Sequence 196 AA;

Query Match Score 718.5; DB 20; Length 196;
Best Local Similarity 74.6%; Pred. No. 3.2e-67;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MIGSRAVMLLILLPPTAQRAVPGSSAWTCQQLSQKLTCLANSAAHPLVGHMD-LREE 59
Db 1 MLDCAVIMLWLLPWTQGLAVPRSSSDWAOCQQLSRNLCMANAHAPAGHMMLRE 60

QY 120 PVAQIHLASLGLSQLQPEGHMWTQIPSLSPQMPQLLRFKTLRSLOAFVAVAARY 179
Db 121 PMEQIHLTSLLGLSQLQPEDHPRTQMPSLSSQQQRPLRSKTLRSLOAFIAARY 180

QY 180 FAHGAATLS 188
Db 181 FAHGAATLF 189

RESULT 11
AAB01982 standard; Protein; 196 AA.

XX DT 27-SEP-2000 (first entry)

XX ID AAB01982

XX DE Murine interleukin-B30 (IL-B30).

XX KW Interleukin-B30; IL-B30; murine; cytokine; cellular signalling;
KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
KW granulocyte colony stimulating factor; immune disorder; inflammatory disease; autoimmune disease; antigen; antibody.

XX AC AAB01982;

Query Match 46.1%; Score 463; DB 20; Length 102;
 Best Local Similarity 90.0%; Pred. No. 9 1e-41;
 Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 89 CLQRHQLIYFYEKLGSDFITGEPSLPPSPVQLHASLIGLSQLQPFGHHWETQIP 148
 Db 2 CLQRHQLIYFYEKLGSDFITGEPSLPPSPVQLHASLIGLSQLQPFGHHWETQIP 61

Qy 149 SISPSQPQRLLRFLKILRSQAFVAVAARVFAHGAAATLS 188
 Db 62 SISPSQPQRLLRFLKILRSQAFVAVAARVFAHGAAATLS 101

RESULT 15

AAB01983 ID AAB01983 standard; Protein: 102 AA.
 XX AC
 XX AAB01983;
 XX DT 27-SEP-2000 (first entry)
 XX DE Mature porcine interleukin-B30 (IL-B30).
 XX KW Interleukin-B30; IL-B30; Porcine; pig; cytokine; cellular signalling;
 XX immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
 XX granulocyte colony stimulating factor; immune disorder;
 XX inflammatory disease; autoimmune disease; antigen; antibody.
 XX OS Sus scrofa.
 XX PN US6060284-A.
 XX PD 09-MAY-2000.
 XX PF 24-JUL-1998; 98US-0122443.
 XX PR 25-JUL-1997; 97US-0053765.
 XX PA (SCHIE) SCHERTING CORP.
 XX DR WPI; 2000-364420/31.
 XX PT Novel recombinant DNA encoding cytokines especially interleukin-B30
 XX PT useful as probes or primers for diagnosing immune disorders including
 XX autoimmune or chronic inflammatory conditions
 XX PS Claim 1; Column 45-46; 32pp; English.

CC This sequence represents porcine interleukin-B30 (IL-B30). IL-B30
 CC is a novel cytokine, exhibiting significant homology to IL-6 and
 CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical
 CC role in signalling between immune or other cells during an immune
 CC response. The precise role if IL-B30 is not yet known - it is likely to
 CC have either a stimulatory or an inhibitory effect on haematopoietic cells
 CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.
 CC Alternatively, it may affect vascular physiology or development, or have
 CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and
 CC antagonists are useful in the diagnosis and treatment of disorders
 CC associated with abnormal expression or activity of IL-B30 e.g.,
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are
 CC useful for recombinant expression of IL-B30 in a host cell, and as a
 CC source of probes and primers. The IL-B30 probes and primers can be used
 CC to detect levels of IL-B30 expression in samples from patients suspected
 CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may
 CC also be used to identify homologous genes in other species. IL-B30
 CC protein or its fragments are useful as antigens for raising antibodies to
 CC various linear and conformational epitopes. Such antibodies may be used
 CC to detect levels of IL-B30 protein in a sample.
 XX Sequence• 102 AA;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:54:30 ; Search time 7.36364 Seconds
(without alignments)
401.978 Million cell updates/sec

Title: US-09-658-699-2

Perfect score: 1004

Sequence: 1 MLGSRAVMLLLEFWTAQGR.....QAFVAVAARYFAHGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Published Applications AA: *

1: /cgn2_6/podata/1/pubpaas/US08_NEW_PUB_pep:*

2: /cgn2_6/podata/1/pubpaas/PCT_NEW_PUB_pep:*

3: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB_pep:*

4: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB_pep:*

5: /cgn2_6/podata/1/pubpaas/US07_PUBCOMB_pep:*

6: /cgn2_6/podata/1/pubpaas/US07_PUBCOMB_pep:*

7: /cgn2_6/podata/1/pubpaas/PCUTS_PUBCOMB_pep:*

8: /cgn2_6/podata/1/pubpaas/US08_PUBCOMB_pep:*

9: /cgn2_6/podata/1/pubpaas/US09_NEW_PUB_pep:*

10: /cgn2_6/podata/1/pubpaas/US09_PUBCOMB_pep:*

11: /cgn2_6/podata/1/pubpaas/US10_NEW_PUB_pep:*

12: /cgn2_6/podata/1/pubpaas/US10_PUBCOMB_pep:*

13: /cgn2_6/podata/1/pubpaas/US60_NEW_PUB_pep:*

14: /cgn2_6/podata/1/pubpaas/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	10.1	175	10	US-09-754-532-80
2	101	10.1	175	10	US-09-754-532-87
3	101	10.1	175	10	US-09-754-532-88
4	101	10.1	175	10	US-09-754-532-97
5	100	10.0	175	10	US-09-754-532-79
6	99	9.9	175	10	US-09-754-532-106
7	98	9.8	175	10	US-09-754-532-90
8	97	9.7	175	10	US-09-754-532-89
9	97	9.7	175	10	US-09-754-532-110
10	96	9.6	174	10	US-09-760-008A-1
11	96	9.6	174	10	US-09-750-473-2
12	96	9.6	174	12	US-10-016-103-1
13	96	9.6	174	12	US-10-016-103-2
14	96	9.6	174	12	US-10-000-495-1
15	96	9.6	175	10	US-09-754-532-2
16	96	9.6	175	10	US-09-754-532-68
17	96	9.6	175	10	US-09-754-532-70
18	96	9.6	175	10	US-09-754-532-78
19	96	9.6	175	10	US-09-754-532-83

ALIGNMENTS

RESULT 1
US-09-754-532-80

; Sequence 80, Application US/09754532
; Patent No. US2001001619A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09-754-532
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-80
Query Match 10.1%; Score 101%; DB 10%; Length 175;

Best Local Similarity 26.6%; Pred. No. 0.046; Mismatches 19; Indels 40; Gaps 9; Matches 49; Conservative 19;

12 LLPWTIAQRGAVPGGSSPAWCQQLSQKLTAWSAHP---LVGHMDLREGDEETND 67
 15 LURKLCQVRKQDGA-----ALOEKIKATYKLCHPEELVLIGH-----SLG 56

Qy 68 VPHIQCGDGPQGLRDNSOFLCIRHQGLIFYEKLGSDFITG-EPSLLPDSPVQAQLHA 126
 57 IPWAPL-SSCPSPQALQ---LAGLCSLHSCLFLQGLL-QALEGISPELGPTLDTQLDV 111

Db 112 ADFTATTIWIQOME---ELGMAPALQPTQGAMPAAFSAFORRAGGVLYVASHQSLEVESYR 167

Qy 127 SLLGSQLLQPEGHWETQIPSLPSQ-----PWQRLLRKFILRSLOQAFYAAVAR 178
 15 LURKLCQVRKQDGA-----ALOEKIKATYKLCHPEELVLIGH-----SLG 56

Db 1168 VLRIH 171

RESULT 3
 US-09-754-532-88
 Sequence 88, Application US/09754532

Patent No. US20010016191A1

GENERAL INFORMATION:
 APPLICANT: Osslund, Timothy D.
 TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 110
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Augen Inc.
 STREET: Augen Center, 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: United States of America
 ZIP: 91320-1789

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/754,532
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/448,716
 ATTORNEY/AGENT INFORMATION:
 NAME: Pessin, Karol
 REGISTRATION NUMBER: 34,899
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805/499-5725
 TELEFAX: 805/499-8011
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/754,532
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/448,716
 ATTORNEY/AGENT INFORMATION:
 NAME: Pessin, Karol
 REGISTRATION NUMBER: 34,899
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805/499-5725
 TELEFAX: 805/499-8011
 INFORMATION FOR SEQ ID NO: 87:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-754-532-88

Query Match 10.1%; Score 101; DB 10; Length 175;
 Best Local Similarity 26.6%; Pred. No. 0.046; Mismatches 19; Indels 40; Gaps 9; Matches 49; Conservative 19;

12 LLPWTIAQRGAVPGGSSPAWCQQLSQKLTAWSAHP---LVGHMDLREGDEETND 67
 15 LURKLCQVRKQDGA-----ALOEKIKATYKLCHPEELVLIGH-----SLG 56

Qy 68 VPHIQCGDGPQGLRDNSOFLCIRHQGLIFYEKLGSDFITG-EPSLLPDSPVQAQLHA 126
 57 IPWAPL-SSCPSPQALQ---LAGLCSLHSCLFLQGLL-QALEGISPELGPTLDTQLDV 111

Qy 127 SLLGSQLLQPEGHWETQIPSLPSQ-----PWQRLLRKFILRSLOQAFYAAVAR 178
 15 LURKLCQVRKQDGA-----ALOEKIKATYKLCHPEELVLIGH-----SLG 56

Db 112 ADFTATTIWIQOME---ELGMAPALQPTQGAMPAAFSAFORRAGGVLYVASHQSLEVESYR 167

Qy 179 VFAH 182
 15 LURKLCQVRKQDGA-----ALOEKIKATYKLCHPEELVLIGH-----SLG 56

Db 168 VLRIH 171

RESULT 4
 US-09-754-532-97

Sequence 97, Application US/09754532
 Patent No. US20010016191A1
 GENERAL INFORMATION:
 APPLICANT: Osslund, Timothy D.
 TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 110
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: Amgen Center, 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: California
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/754,532
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/448,716
 ATTORNEY/AGENT INFORMATION:
 NAME: Pessin, Karol
 REGISTRATION NUMBER: 34,899
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805/499-5725
 TELEFAX: 805/499-8011
 INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-754-532-97

Query Match 10.1; Score 101; DB 10; Length 175;
 Best Local Similarity 26.6%; Pred. No. 0.0046;
 Matches 49; Mismatches 76; Indels 40; Gaps 9;

QY 12 LIPWTAQGRAVPGSSPAWTQCOQLSQKICLANSAAHP---LYGHMDLREQDEETND 67
 Db 15 LRLCLDVRKIQDGAA-----ALQEKLCATYKICHPBBLVIGH-----SLG 56
 QY 68 VPHIQCGDGGCDPQGLRNSQCLQRHQGLIFYEKLGSDFIIG-EPSLIPDSPVAQHLA 126
 Db 57 IPWAPL-SSCP-SQALQ--LAGCLSQLHSGLFLYQGLL--QALEGISPEGLTDLTQLDV 111
 QY 127 SLGLSQLLQPESHHWETQQLPSLSQ-----PMORLLRFKILRSQAFAVAAAR 178
 Db 112 ADFTATTWQME---ELGMAPALQOPTQGAMPAPASAFOARRAGGVLYASHLQSFLVEYSR 167
 QY 179 VFAHGA 185
 Db 168 VLRLHAA 174

RESULT 6
 US-09-754-532-106
 Sequence 106, Application US/09754532
 Patent No. US20010016191A1
 GENERAL INFORMATION:
 APPLICANT: Osslund, Timothy D.
 TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 110
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: Amgen Center, 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: California

COUNTRY: United States of America
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/754,532
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/448,716
 ATTORNEY/AGENT INFORMATION:
 NAME: Pessin, Karol
 REGISTRATION NUMBER: 34,899
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805/499-5725
 TELEFAX: 805/499-8011
 INFORMATION FOR SEQ ID NO: 79:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-754-532-79

Query Match 10.0%; Score 100; DB 10; Length 175;
 Best Local Similarity 26.7%; Pred. No. 0.0058;
 Matches 50; Conservative 19; Mismatches 78; Indels 40; Gaps 9;

QY 12 LIPWTAQGRAVPGSSPAWTQCOQLSQKICLANSAAHP---LYGHMDLREQDEETND 67
 Db 15 LRLCLDVRKIQDGAA-----ALQEKLCATYKICHPBBLVIGH-----SLG 56
 QY 68 VPHIQCGDGGCDPQGLRNSQCLQRHQGLIFYEKLGSDFIIG-EPSLIPDSPVAQHLA 126
 Db 57 IPWAPL-SSCP-SQALQ--LAGCLSQLHSGLFLYQGLL--QALEGISPEGLTDLTQLDV 111
 QY 127 SLGLSQLLQPESHHWETQQLPSLSQ-----PMORLLRFKILRSQAFAVAAAR 178
 Db 112 ADFTATTWQME---ELGMAPALQOPTQGAMPAPASAFOARRAGGVLYASHLQSFLVEYSR 167
 QY 179 VFAHGA 185
 Db 168 VLRLHAA 174

RESULT 6
 US-09-754-532-106
 Sequence 106, Application US/09754532
 Patent No. US20010016191A1
 GENERAL INFORMATION:
 APPLICANT: Osslund, Timothy D.
 TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
 NUMBER OF SEQUENCES: 110
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: Amgen Center, 1840 DeHavilland Drive
 CITY: Thousand Oaks
 STATE: California

COUNTRY: United States of America
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/754,532
 FILING DATE:
 CLASSIFICATION:

Db 15 LKKCQVKRKGAGA-----ALQEKLCATYKLCHPEELVUGH-----SLG 56
 Qy 68 VPHIQCGDGGDPGLRDNSSCOPQRHQLIYKLLGSDIFTG-EPSLLPDSPVQHLA 126
 Db 57 IPWAPL-SSCP\$QALQ-LAGCLSQLHSGLSFLYQGLL--QALEGTSPLEGPTDLQLDV 111
 Qy 127 SLIGLSQLQPEGHWTQQPLSPLSPQ-----PWRQLLRFKLRSQAFQAVAYAR 178
 Db 112 ADFTATIWQOME---ELGMAPALQPTQGAMPFAFASAFQRAGGVLYASHLQSLEYSYR 167
 Qy 179 VFAH 182
 Db 168 VLRH 171

RESULT 9
 US-09-754-532-110
 ; Sequence 110, Application US/09754532
 ; Patent No. US20010016191A1
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Ossland, Timothy D.
 ; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 110
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: Abgen Center, 1840 DeHavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; APPLICATION NUMBER: US/09/754,532
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/448,716
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ;
 ; NAME: Pessin, Karol
 ; REGISTRATION NUMBER: 34,899
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 805/499-5725
 ; TELEFAX: 805/499-8011
 ; INFORMATION FOR SEQ ID NO: 110:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 175 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQ ID NO: 110

Query Match 9.68; Score 96; DB 10; Length 174;
 Best Local Similarity 26.1%; Pred. No. 0.015; Indels 40; Gaps 9;
 Matches 48; Conservative 20; Mismatches 19; Mismatches 77; Indels 40; Gaps 9;

Db 14 LLKCLEQVRKIQGDGA-----ALQEKLCAKYKLCHPEELVUGH-----SLG 55
 Qy 12 LLPRTAQGRAVPGGSSPAWTCQQLSQKLTLAASHP---LVGHMDIREEGDEETND 67
 Db 56 IPWAPL-SSCP\$QALQ-LAGCLSQLHSGLSFLYQGLL--QALEGTSPLEGPTDLQLDV 111
 Qy 127 SLIGLSQLQPEGHWTQQPLSPLSPQ-----PWRQLLRFKLRSQAFQAVAYAR 178
 Db 111 ADFTATIWQOME---ELGMAPALQPTQGAMPFAFASAFQRAGGVLYASHLQSLEYSYR 166
 Qy 179 VFAH 182
 Db 167 VLRH 170

Query Match 9.7%; Score 97; DB 10; Length 175;
 Best Local Similarity 26.1%; Pred. No. 0.012; Indels 40; Gaps 9;
 Matches 48; Conservative 20; Mismatches 20; Mismatches 76; Indels 40; Gaps 9;

Db 15 LKKCQVKRKGAGA-----ALQEKLCATYKLCHPEELVUGH-----SLG 56
 Qy 68 VPHIQCGDGGDPGLRDNSSCOPQRHQLIYKLLGSDIFTG-EPSLLPDSPVQHLA 126
 Db 57 IPWAPL-SSCP\$QALQ-LAGCLSQLHSGLSFLYQGLL--QALEGTSPLEGPTDLQLDV 111
 Qy 127 SLIGLSQLQPEGHWTQQPLSPLSPQ-----PWRQLLRFKLRSQAFQAVAYAR 178
 Db 112 ADFTATIWQOME---ELGMAPALQPTQGAMPFAFASAFQRAGGVLYASHLQSLEYSYR 167

;

LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-09-950-473-2

Query Match 9.6%; Score 96; DB 10; Length 174;
Best Local Similarity 26.1%; Pred. No. 0.015; Mismatches 19; Indels 40; Gaps 9;
Matches 48; Conservative

Qy 12 LLPWTAQGRAVPGGSSPANTOCOOLSQLKICLTLWAHP---LYGHMDLRLERGDEETIND 67
Db 14 LLKCCLCQVRKIQGDGA----ALQEKLICATYKLCHPEELVLIGH-----SLG 55

Qy 18 VPHIQCGDGDPOGLRDNDSLCTHOSFYKLGSDIFTG-EPSLLPDSPVAQLHA 126
Db 56 IPWAPL-SSCPSQLAQ--LAGCISQLHSFLFLYQGLL-QALEGISPLGLPQTDLQDV 110

Qy 127 SLLGSQLQIQLQEPGHHWETQOIPSLSPSQ-----PWQRLLRFKILRSQAFAYAAR 178
Db 111 ADFAFTIWQOME---ELGMAPALQPTQGAMPAAFASAORRAGGVLYASHLQSLEVSYR 166

Qy 179 VFAH 182
Db 167 VLRH 170

RESULT 13
US-10-016-403-2
Sequence 2, Application US/10016403
; Patent No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Holladay, Leslie A.
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patientin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIORITY DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 10-Dec-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..174
; OTHER INFORMATION: /note= "modified granulocyte-colony
; stimulating factor"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-016-403-2

Query Match 9.6%; Score 96; DB 12; Length 174;
Best Local Similarity 26.1%; Pred. No. 0.015; Mismatches 19; Indels 40; Gaps 9;
Matches 48; Conservative

QY 12 LIPWTAQGRAVPGGSSPAWCQQQLSOKLCTLAWSAHP---LVGHMDLREGDEETND 67
 ||| :||| :||| :||| :||| :||| :||| :|||
 Db 14 LURCLEYRKIQGDGA-----ALQEKUCATYKLCHBEELVLGH-----SLG 55

QY 68 VPHIQCQDGCDPQGLRDNQSFCQLRIHQGLIFYEKLGSDFITG -EPSLLPDSPVQQLHA 126
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 56 IPWAPL-SSCP(SQALQ-LAGCLSLQHSGFLYQGLL-QALEGISPELGLTDLQLDV 110
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 127 SLIGLSOLLOPQEGHHMETQQIPSPSQ-----PQRLRLRFKFLRSQAFYAVVAR 178
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 111 ADFATTIWQMB---ELGMAPALOPTQGAMPAPAFASAQRAGGVLYASHLQSFLVEYSR 166
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 179 VFAH 182
 ||| :|||
 Db 167 VLRH 170

RESULT 14
 US-10-003-496-1
 ; Sequence 1, Application US/10003496
 ; Patent No. US20020142964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maxygen ApS
 ; APPLICANT: Maxygen Holdings Ltd.
 ; TITLE OF INVENTION: Single-Chain Polypeptides
 ; FILE REFERENCE: 0318US210
 ; CURRENT APPLICATION NUMBER: US/10/003,496
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/245,727
 ; PRIOR FILING DATE: 2000-11-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-003-496-1

Query Match 9 6%; Score 96; DB 12; Length 174;

Best Local Similarity 26.18; Pred. No. 0.015; Mismatches 19; Indels 40; Gaps 9;
 Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 12 LIPWTAQGRAVPGGSSPAWCQQQLSOKLCTLAWSAHP---LVGHMDLREGDEETND 67
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 14 LURCLEYRKIQGDGA-----ALQEKUCATYKLCHBEELVLGH-----SLG 55

QY 68 VPHIQCQDGCDPQGLRDNQSFCQLRIHQGLIFYEKLGSDFITG -EPSLLPDSPVQQLHA 126
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 56 IPWAPL-SSCP(SQALQ-LAGCLSLQHSGFLYQGLL-QALEGISPELGLTDLQLDV 110
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 127 SLIGLSOLLOPQEGHHMETQQIPSPSQ-----PQRLRLRFKFLRSQAFYAVVAR 178
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 111 ADFATTIWQMB---ELGMAPALOPTQGAMPAPAFASAQRAGGVLYASHLQSFLVEYSR 166
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 179 VFAH 182
 ||| :|||
 Db 167 VLRH 170

RESULT 15

US-09-754-532-2
 ; Sequence 2, Application US/09754532

; Patent No. US20010016191A1
 ; GENERAL INFORMATION:

; APPLICANT: Osslund, Timothy D.

; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS

; NUMBER OF SEQUENCES: 110
 ; CORRESPONDENCE ADDRESS:

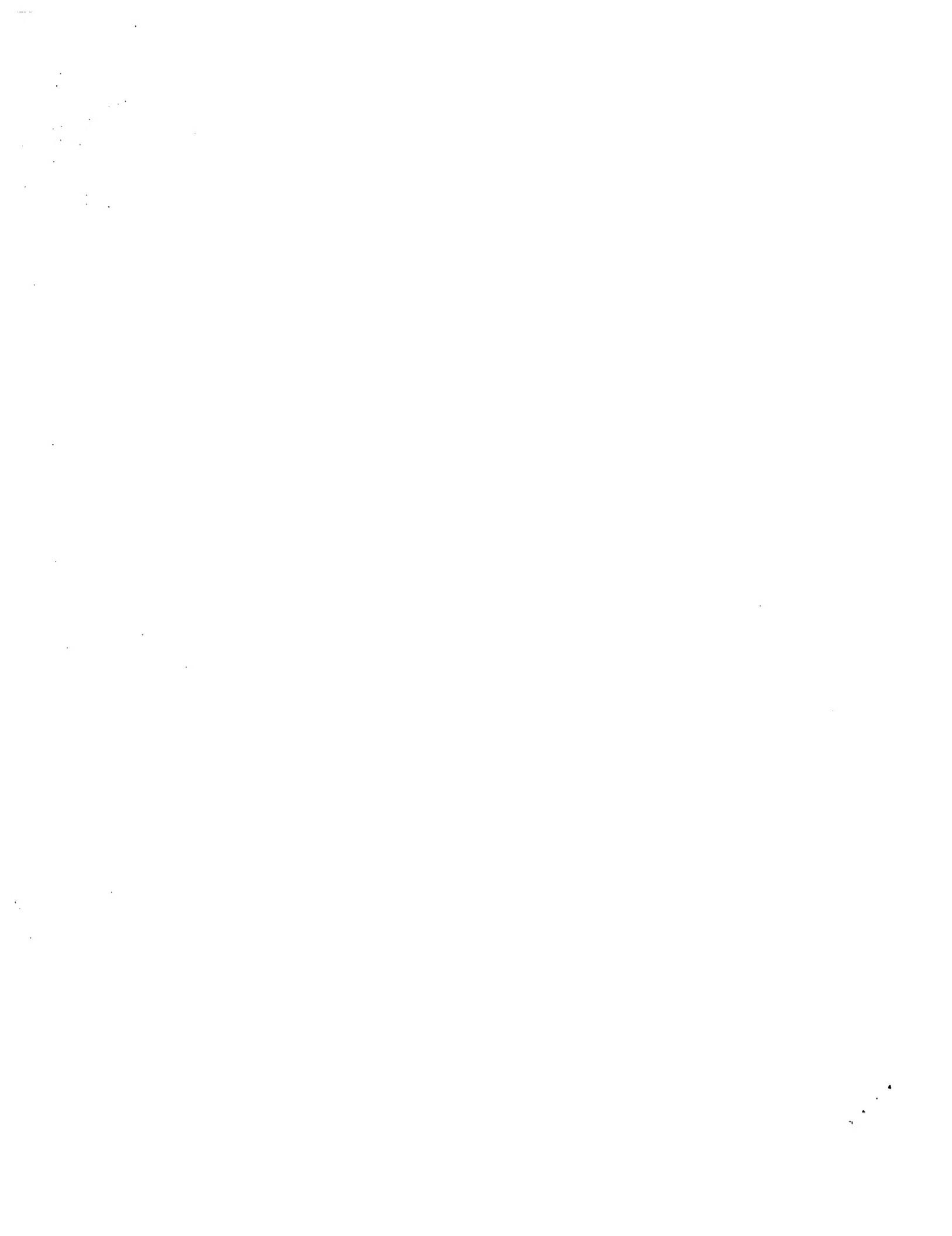
; ADDRESSEE: Angen Inc.

; STREET: Thousand Oaks, 1840 DeHavilland Drive

; CITY: California

Search completed: November 20, 2002, 12:00:55
 Job time : 8.36334 secs

COUNTRY: United States of America
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/754,532
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/448,716
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Pessin, Karol
 REGISTRATION NUMBER: 34,899
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 805/499-5725
 TELEFAX: 805/499-8011
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-754-532-2
 Query Match 9 6%; Score 96; DB 10; Length 175;
 Best Local Similarity 26.18; Pred. No. 0.015; Mismatches 19; Indels 40; Gaps 9;
 Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;
 QY 12 LLWTAQRAVPGGSSPAWCQQQLSOKLCTLAWSAHP---LVGHMDLREGDEETND 67
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 15 LURCLEYRKIQGDGA-----ALQEKUCATYKLCHBEELVLGH-----SLG 56
 QY 68 VPHIQCQDGCDPQGLRDNQSFCQLRIHQGLIFYEKLGSDFITG -EPSLLPDSPVQQLHA 126
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 57 IPWAPL-SSCP(SQALQ-LAGCLSLQHSGFLYQGLL-QALEGISPELGLTDLQLDV 111
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 127 SLIGLSOLLOPQEGHHMETQQIPSPSQ-----PQRLRLRFKFLRSQAFYAVVAR 178
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 112 ADFATTIWQME---ELGMAPALOPTQGAMPAPAFASAQRAGGVLYASHLQSFLVEYSR 167
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 179 VFAH 182
 ||| :|||
 Db 168 VLRH 171



GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

1 protein - protein search, using sw mode!

on on: November 20, 2002, 11:53:05 ; Search time 11.7818 Seconds
(without alignments)
471.993 Million cell updates/sec

Title: US-09-658-699-2
Perfect score: 1004
Sequence: 1: MIGSRAYMLLILPPTAQGR.....QAFVAVAVARVFAHGAATLSP 189
Scoring table: BLOSUM62
Gapext 0.0 , Gapext 0.5

Searched: 262574 seqs, 2942922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

database : Issued_Patents_AA:*

1: /cgn2_6_ptodata/1/iaa/5A_COMBO.pep:*

2: /cgn2_6_ptodata/1/iaa/5B_COMBO.pep:*

3: /cgn2_6_ptodata/1/iaa/6A_COMBO.pep:*

4: /cgn2_6_ptodata/1/iaa/6B_COMBO.pep:*

5: /cgn2_6_ptodata/1/iaa/PCTUS_COMBO.pep:*

6: /cgn2_6_ptodata/1/iaa/backtfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	1004	100.0	189	3	US-09-122-443-2		Sequence 2, Appli
2	718.5	71.6	196	3	US-09-122-443-4		Sequence 4, Appli
3	463	46.1	102	3	US-09-122-443-5		Sequence 5, Appli
4	102	10.2	307	3	US-08-469-318-121		Sequence 121, App
5	102	10.2	307	3	US-08-469-318-122		Sequence 122, App
6	102	10.2	307	3	US-08-469-318-134		Sequence 134, App
7	102	10.2	307	3	US-08-469-619-135		Sequence 135, App
8	102	10.2	307	3	US-08-468-609A-121		Sequence 121, App
9	102	10.2	307	3	US-08-468-609A-122		Sequence 122, App
10	102	10.2	307	3	US-08-468-609A-134		Sequence 134, App
11	102	10.2	307	3	US-08-468-609A-135		Sequence 135, App
12	102	10.2	307	4	US-08-446-872A-121		Sequence 121, App
13	102	10.2	307	4	US-08-446-872A-122		Sequence 122, App
14	102	10.2	307	4	US-08-46-72A-134		Sequence 134, App
15	102	10.2	307	4	US-08-446-872A-135		Sequence 135, App
16	102	10.2	307	4	US-08-762-227A-121		Sequence 121, App
17	102	10.2	307	4	US-08-762-227A-122		Sequence 122, App
18	102	10.2	307	4	US-08-762-227A-134		Sequence 134, App
19	102	10.2	307	4	US-08-762-227A-135		Sequence 135, App
20	102	10.2	307	5	PCT-US95-01185-121		Sequence 121, App
21	102	10.2	307	5	PCT-US95-01185-122		Sequence 122, App
22	102	10.2	307	5	PCT-US95-01185-134		Sequence 134, App
23	102	10.2	307	5	PCT-US95-01185-135		Sequence 135, App
24	101	10.1	175	1	US-08-010-099-80		Sequence 80, Appli
25	101	10.1	175	1	US-08-010-099-81		Sequence 81, Appli
26	101	10.1	175	1	US-08-010-099-82		Sequence 82, Appli
27	101	10.1	175	1	US-08-010-099-83		Sequence 83, Appli

ALIGNMENTS

RESULT 1
US-09-122-443-2
Sequence 2, Application US/09122443
Patent No. 600284
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: DNAX Research Institute
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94041-1104
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122, 443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053, 765
FILING DATE: 10-7-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)952-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-122-443-2

Query Match Best Local Similarity 100.0%; Score 1004; DB 3; Length 189;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MGSRAYMLLILPPTAQGRAVPGGSPTAWTOCQLSOKLTLAWSHPLVGHMDLREG 60
Db 1 MGSRAYMLLILPPTAQGRAVPGGSPTAWTOCQLSOKLTLAWSHPLVGHMDLREG 60

Db	181 FAHCATLT 189	RESULT 3 US-09-122-443-5 ; Sequence 5, Application ; Patent No. 6060284 ; GENERAL INFORMATION: ; APPLICANT: Bazzan, ; TITLE OF INVENTION: ; NUMBER OF SEQUENCE ; CORRESPONDENCE ADDRESSEES: ; ADDRESSEE: DNAX ; STREET: 901 Cal. ; CITY: Palo Alto ; STATE: California ; COUNTRY: USA ; ZIP: 94304-1104 ; COMPUTER READABLE ; MEDIUM TYPE: FILE ; COMPUTER: IBM PC ; OPERATING SYSTEM: ; SOFTWARE: Patent ; CURRENT APPLICATION ; APPLICATION NUMBER: ; FILING DATE: 24 ; CLASSIFICATION: ; PRIORITY APPLICATION ; APPLICATION NUMBER: ; FILING DATE: 25 ; ATTORNEY/AGENT INFO ; NAME: Ching, Ed ; REGISTRATION NUMBER: ; REFERENCE/DOCKET ; TELECOMMUNICATION ; TELEPHONE: (650) ; TELEFAX: (650) 94 ; INFORMATION FOR SEQ ; SEQUENCE CHARACTER ; LENGTH: 102 amino ; TYPE: amino acid ; STRANDEDNESS: n ; TOPOLOGY: linear ; MOLECULE TYPE: peptide ; US-09-122-443-5
		Query Match Best Local Similarity Matches 90; Consen-
Qy	89	CLQRTHQGLLIVF
Db	2	CLQRTHQGLVLFYV
Qy	149	STSPSQPWRQLLII
Db	62	SPSPSQPWRQLLII
		RESULT 4 US 08-469-318-121 ; Sequence 121, Application ; Patent No. 602235 ; GENERAL INFORMATION: ; APPLICANT: ; TITLE OF INVENTION: ; NUMBER OF SEQUENCE ; COMPUTER READABLE ; MEDIUM TYPE: FILE ; COMPUTER: IBM PC ; OPERATING SYSTEM: ; SOFTWARE: Patent

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
MS-08/469-318-121

Query Match	Score	DB 3;	Length	307;
Best Local Similarity	24.8%	Pred. No.	0.0016;	
Matches	52;	Conservative	22;	Mismatches 74;
Indels	62;	Gaps		
15 WTAQGRAVPGGS	-	-	-	-
:			PAWT	-
114 YVIEGRISPGGGSGGSNNATAPGPPASSPLPQSFLKCLEQYRKLOGDGAQALQEKLCAKY	173	:	:	LSQMLCTLAW 45
46 SAHP ---LYGHMDLRECGDEETTNVDPHIQCGDGCQPLQLRDNQSFCLORIHQGLIYFE	101	:	:	:
174 LCHPEELVLIGH-----SLGIPWPWAL-SSCPSQALQ--LAGCULSQHSLGFLFYQ	219	:	:	:
102 KLGSDIFG-EPSLLPDPSPVAGLHASLLGSQLLOPPEGHWWETQPLSPLSPS---	154	:	:	:
220 GLR - QALEGISPLGPTLDLCLDVADEATTWQOME---ELGMAPALQPTQGAMPAF	273	:	:	:
155 -PQORLLRFKFLRSQGAFVANAARYFAH 182		:	:	
274 ASAFTORRAGGVLYVASHQLOSEFESYRILH		:	:	

RESULT 5
-08-08-469-318-122 Sequence 122; Application US/08469318
Patent No. 60/22535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivarient IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469, 318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446, 872
FILING DATE:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-08-469-318-122 Query Match 10.2%; Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 20; Mismatches 76; Indels
15 WTAQGRAVPGGSS-----PAWTQCCQ-----1-SOK

RESULT 6
US-08-469-318-134 Application US/08469318
Sequence 1-34, Application US/08469318
Patent No. 6022535

GENERAL INFORMATION:

APPLICANT: TITLE OF INVENTION: Multivarient IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08469, 318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIORITY NUMBER: 08/1446 872
ADDITIONAL NUMBER:

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,609A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/192,325
 FILING DATE: 14-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C-2790/3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 737-6986
 TELEFAX: (314) 737-6972
 INFORMATION FOR SEQ ID NO: 121:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 307 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-468-609A-121

Query Match 10.2%; Score 102; DB 3; Length 307;
 Best Local Similarity 24.8%; Pred. No. 0.0016;
 Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

Y	15	WTAQGRAYPGSS-----PAWTQCOQ-----LSQKLCTLAW 45
Db	114	YVTECRISPGGSGGGNNATPLGPASSPLPQSPFLILKSLDQVRKIQGDDQALQELKICATYK 173
Dy	46	SAHP----LVGHMDLREEGDEETNDVPHIQCQGCDPGLRDNNSQFCQLRTHQGLLIFYE 101
Db	174	IChPEELVLIGH-----SUGIPWAPL-SSCPSCAQ-LAGGLSQHSGLFLYQ 219
Dy	102	KLLGSDIFTG-EPSLLPDSVAQHLSLGLSQQLQPESHHWETQIPSLSSQ----- 154
Db	220	GIL---QALEGISPSLEGPTDLTQDVAFTIWQME---ELGMAPALQPTQGAMPAF 273
Dy	155	-PWQRLLRFKILRSLSQAFAVAVARVFAH 182
Db	274	ASAFQRAGGVLVASHLQSFLEVSTRVLRH 303

Query Match 10.2%; Score 102; DB 3; Length 307;
 Best Local Similarity 24.8%; Pred. No. 0.0016;
 Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

Qy	15	WTAQGRAYPGSS-----PAWTQCOQ-----LSQKLCTLAW 45
Db	114	YVTECRISPGGSGGGNNATPLGPASSPLPQSPFLILKSLDQVRKIQGDDQALQELKICATYK 173
Qy	46	SAHP----LVGHMDLREEGDEETNDVPHIQCQGCDPGLRDNNSQFCQLRTHQGLLIFYE 101
Db	174	IChPEELVLIGH-----SUGIPWAPL-SSCPSCAQ-LAGGLSQHSGLFLYQ 219
Qy	102	KLLGSDIFTG-EPSLLPDSVAQHLSLGLSQQLQPESHHWETQIPSLSSQ----- 154
Db	220	GIL---QALEGISPSLEGPTDLTQDVAFTIWQME---ELGMAPALQPTQGAMPAF 273
Qy	155	-PWQRLLRFKILRSLSQAFAVAVARVFAH 182
Db	274	ASAFQRAGGVLVASHLQSFLEVSTRVLRH 303

RESULT 8
 US-08-468-609A-121 ; Sequence 121, Application US/08468609A
 ; GENERAL INFORMATION:
 ; APPLICANT: Abrams, Mark A.
 ; APPLICANT: Bauer, S. C.
 ; APPLICANT: Bradford-Coldberg, Sarah R.
 ; APPLICANT: Caparon, Maire H.
 ; APPLICANT: Easton, Alan M.
 ; APPLICANT: Klein, Barbara K.
 ; APPLICANT: McKearn, John P.
 ; APPLICANT: Olius, Peter O.
 ; APPLICANT: Paik, Kumaran
 ; APPLICANT: Thomas, John W.
 ; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-11)
 ; NUMBER OF SEQUENCES: 197
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 ; STREET: P. O. Box 5110
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60680
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 9
 US-08-468-609A-122 ; Sequence 122, Application US/08468609A
 ; GENERAL INFORMATION:
 ; APPLICANT: Abrams, Mark A.
 ; APPLICANT: Bauer, S. C.
 ; APPLICANT: Bradford-Coldberg, Sarah R.
 ; APPLICANT: Caparon, Maire H.
 ; APPLICANT: Easton, Alan M.
 ; APPLICANT: Klein, Barbara K.
 ; APPLICANT: McKearn, John P.
 ; APPLICANT: Olius, Peter O.
 ; APPLICANT: Paik, Kumaran
 ; APPLICANT: Thomas, John W.
 ; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-11)
 ; NUMBER OF SEQUENCES: 197
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 ; STREET: P. O. Box 5110
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60680
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,609A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/192,325
 FILING DATE: 14-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C-2790/3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)737-6986
 TELEFAX: (314)737-6972
 INFORMATION FOR SEQ ID NO: 122:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 307 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQ ID NO: 122
 5'-08-468-609A-122

Query Match Score 102; DB 3; Le⁺
 Best Local Similarity 24.8%; Fred. No. 0.0016;
 Matches 52; Conservative 20; Mismatches 76;

15 WTAQGRAVPGSSS-----PAWTQCOQ-----	114 YVIEGRISPGGGSGGSNNMPLGEASSLQPSQSFLLKSLEQVQRKIQ-----
/	46 SAHP ---LYGHMDLREEGDEETTDVPHIQCNGCDPQGLRDNSS-----
o	174 LCHPEEVLGLH-----SLIGIPWAPL-SSCPSPALQ -L-----
/	102 KULGSDIFTG-EPSSLQDPSVPAQLHASLIGLSQLQPEGHHWETQ-----
o	220 GLL--QALEGSPERGPDTDLQLVADFATTIWQME---B1G3-----
/	155 --PWQRLLLRKILRSLSQAVAVAVARVFH 182
o	274 ASAQQRRAGGYLVASHLQSFLVESTRVLRH 303

RESULT 10
 5'-08-468-609A-134
 Sequence 134, Application US/08468609A
 Patent No. 6030812
 GENERAL INFORMATION:
 APPLICANT: Abrams, Mark A.
 APPLICANT: Bauer, S. C.
 APPLICANT: Bradford-Goldberg, Sarah R.
 APPLICANT: Caparon, Maire H.
 APPLICANT: Easton, Alan M.
 APPLICANT: Klein, Barbara K.
 APPLICANT: McKearn, John P.
 APPLICANT: Ollins, Peter Q.
 APPLICANT: Paik, Kunman
 APPLICANT: Thomas, John W.
 TITLE OF INVENTION: Fusion Proteins Comprising Mu
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.
 ADDRESS: Corporate Patent Dept.
 STREET: P. O. Box 5110
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60650
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in-Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-609A-134

Query Match          Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016; Gaps 11;
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

Qy  15 WTAQGAVPGSS--PWT-----PAWT-----OCQQ-----AQKQLCTLAW 45
Db  114 YVIEGRISPGGGGGGSNNMATPLGPASSPLPOSFLLKCLEVRKIQGDGAALQEKLCTAYK 173
Qy  46 SAHP---LYGHMDLREEGDEETNDVPHIQCGDQGDPQHLDNSQFCLOTRIHOGLIFYE 101 .
Db  174 LCHPEEVNLVLRH----SLSITPWL-SSSPSQALQ--LAGCSSLHSGFLFLQ 219
Qy  102 KLLGSDIFTG-EPSLILPDSVPAQLHASLGLSQLQPEGHHWETQOIPSLSPSQ----- 154
Db  220 GLL--@ALEGISPELSPDTLQLDADFTTIIWQO---ELGMAPALQPTQGAMPAF 273
Qy  155 --P@QBLIRKILRSLSQAFYAAVARVEFH 182
Db  274 ASAFOQRAGGVLVASHLQSFFLEVSYRVLRH 303

RESULT 11
US-08-468-609A-135
Sequence 135, Application US/08466609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Braford-Goldberg, Sarah R.
APPLICANT: Bauer, S. C.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kumanan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60660
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,609A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/192,325
 FILING DATE: 14-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C-2790/3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)737-6986
 TELEX/FAX: (314)737-6972
 INFORMATION FOR SEQ ID NO: 135:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 307 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08/468-609A-135

Query Match 10.2%; Score 102; DB 3; Length 307;
 Best Local Similarity 24.8%; Pred. No. 0.0016;
 Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

Qy 15 WTAQGRAVPGGSS-----PAWTOCQQ-----LSOKLCTLAW 45
 Db 114 YVIEGRISPGGGGSNNMATTPLGQASSPQSFLKSLEQVRKLGDSAAALQEKLCTAYK 173
 Qy 46 SAHP---LYGHMDLREEGDEETNDVPHIQCGDQCDPQGLRDNSOFLCLQRTHQGLIIFYE 101
 Db 174 LCHPEBLVLGH-----SLGIPWAPL-SSCPSSOALQ-LAGGLSQHSGSLFLYQ 219
 Qy 102 KLLGSDIFTG-EPSLLPDSVVAQLHSASLLGSQLQPEGHHWETQQTSLSPSQ---- 154
 Db 220 GLL--QALEGISPEGLPTLQLQDVFATIWIQME---ELGMAPALQPTQGAMPAF 273
 Qy 155 --PWQRILLRKILRSQAVAVARVFAH 182
 Db 274 ASAFOQRAGGVLYASHLQSFLEVSYRLRH 303

RESULT 12
 US-08-446-872A-121
 ; sequence 121, Application US/08446872A
 ; Patent No. 6361977
 ; GENERAL INFORMATION:
 ; APPLICANT: Abrams, Mark A.
 ; APPLICANT: Bauer, S. C.
 ; APPLICANT: Bradford-Goldberg, Sarah R.
 ; APPLICANT: Caparon, Maire H.
 ; APPLICANT: Easton, Alan M.
 ; APPLICANT: Klein, Barbara K.
 ; APPLICANT: McKearn, John P.
 ; APPLICANT: Ollins, Peter O.
 ; APPLICANT: Paik, Kumanan
 ; APPLICANT: Thomas, John W.
 ; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
 ; NUMBER OF SEQUENCES: 197
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 ; ADDRESSEE: Corporate Patent Dept.
 ; STREET: P. O. Box 5110
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA

ZIP: 60680
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,872A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/192,325
 FILING DATE: 14-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C-2790/1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314)737-6986
 TELEX/FAX: (314)737-6972
 INFORMATION FOR SEQ ID NO: 121:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 307 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-446-872A-121

Query Match 10.2%; Score 102; DB 4; Length 307;
 Best Local Similarity 24.8%; Pred. No. 0.0016;
 Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

Qy 15 WTAQGRAVPGGSS-----PAWTOCQQ-----LSOKLCTLAW 45
 Db 114 YVIEGRISPGGGGSNNMATTPLGQASSPQSFLKSLEQVRKLGDSAAALQEKLCTAYK 173
 Qy 46 SAHP---LYGHMDLREEGDEETNDVPHIQCGDQCDPQGLRDNSOFLCLQRTHQGLIIFYE 101
 Db 174 LCHPEBLVLGH-----SLGIPWAPL-SSCPSSOALQ-LAGGLSQHSGSLFLYQ 219
 Qy 102 KLLGSDIFTG-EPSLLPDSVVAQLHSASLLGSQLQPEGHHWETQQTSLSPSQ---- 154
 Db 220 GLL--QALEGISPEGLPTLQLQDVFATIWIQME---ELGMAPALQPTQGAMPAF 273
 Qy 155 --PWQRILLRKILRSQAVAVARVFAH 182
 Db 274 ASAFOQRAGGVLYASHLQSFLEVSYRLRH 303

RESULT 13
 US-08-446-872A-122
 ; Sequence 122, Application US/08446872A
 ; Patent No. 6361977
 ; GENERAL INFORMATION:
 ; APPLICANT: Abrams, Mark A.
 ; APPLICANT: Bauer, S. C.
 ; APPLICANT: Bradford-Goldberg, Sarah R.
 ; APPLICANT: Caparon, Maire H.
 ; APPLICANT: Easton, Alan M.
 ; APPLICANT: Klein, Barbara K.
 ; APPLICANT: McKearn, John P.
 ; APPLICANT: Ollins, Peter O.
 ; APPLICANT: Paik, Kumanan
 ; APPLICANT: Thomas, John W.
 ; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
 ; NUMBER OF SEQUENCES: 197
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 ; ADDRESSEE: Corporate Patent Dept.
 ; STREET: P. O. Box 5110
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA

STATE: Illinois
COUNTRY: USA
ZIP: 60660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6986
TELEPHONE: (314)737-6972
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-446-872A-122

Query Match 10 2%; Score 102; DB 4; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016; Gaps 10;
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

Qy 15 WTAQGRAVPGGSS-----PAWTQCOQ---- -LSQRKLTAW 45
Db 114 YVIECRISPGGGGGSNMATPLGPASSPQSFLIKSLFQVRKTQGDGAALQEKLCKY K 173
Qy 46 SAHP ---LVGHMDLREEDDEETNDVPIQCGDPOGLRDNQSQFLQORTHQGLIFYE 101
Db 174 LCHPEELVLIGH-----SIGIPNAPL SSCPSQALQ -LAGLSQDHSGLFLYQ 219
Qy 102 KLLGSDIFG -EPSLLPDSPVAQLHASLIGLSSLQQLPREGHHNETQQIPSLSPSQ----- 154
Db 220 GIL -QALEGSISPLGLQDVAFTTQWQME ---ELGMAPALQPTQGAMPAF 273
Qy 155 -PWORLIRFKILRSQAFVAYAARVFH 182
Db 274 ASAFAARRGCVLIVASHLQSFLEVSYVLRH 303

RESULT 14
US-08-446-872A-134
Sequence 134, Application US/08446872A
Patent No. 6361977

GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kumman
APPLICANT: Thomas, John W.

TITLE OF INVENTION: Multivarient IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.

STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-446-872A-134

Query Match 10 2%; Score 102; DB 4; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016; Gaps 10;
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

Qy 15 WTAQGRAVPGGSS-----PAWTQCOQ---- -OCOO-----LSQRKLTAW 45
Db 114 YVIECRISPGGGGGSNMATPLGPASSPQSFLIKSLFQVRKTQGDGAALQEKLCKY K 173
Qy 46 SAHP ---LVGHMDLREEDDEETNDVPIQCGDPOGLRDNQSQFLQORTHQGLIFYE 101
Db 174 LCHPEELVLIGH-----SIGIPNAPL SSCPSQALQ -LAGLSQDHSGLFLYQ 219
Qy 102 KLLGSDIFG -EPSLLPDSPVAQLHASLIGLSSLQQLPREGHHNETQQIPSLSPSQ----- 154
Db 174 LCHPEELVLIGH-----SIGIPWAPL -SSCPSQALQ -LAGLSQDHSGLFLYQ 219
Qy 102 KLLGSDIFG -EPSLLPDSPVAQLHASLIGLSSLQQLPREGHHNETQQIPSLSPSQ----- 154
Db 220 GIL -QALEGSISPLGLQDVAFTTQWQME ---ELGMAPALQPTQGAMPAF 273
Qy 155 -PWQRLIRFKILRSQAFVAYAARVFH 182
Db 274 ASAFAARRGCVLIVASHLQSFLEVSYVLRH 303

RESULT 15
US-08-446-872A-135
Sequence 135, Application US/08446872A
Patent No. 6361977

GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Ollins, Peter O.
APPLICANT: Paik, Kumman
APPLICANT: Thomas, John W.

TITLE OF INVENTION: Multivarient IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

Page 8

ADDRESSEE: Dennis A. Bennett, G.D. Searie & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 307 amino acids
STRANDEDNESS:
TOPOLOGY: linear
LOCUS: 1-307
VERSION: 1.0

search completed: November 20, 2002, 12:00:12
search time : 13.7818 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:35 ; Search time 14.7636 Seconds
(without alignments)
1276.267 Million cell updates/sec

Title: US-09-658-699-4
Perfect score: 1038
Sequence: 1 MLDICRAYTMLNLPWYQGL.....AARYFAHGAATLTPFLVPTA 196

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	10.9	208	T09216	interleukin-6 prec
2	110	10.6	208	A29549	interleukin-6 prec
3	104	10.0	208	A56610	interleukin-6 prec
4	101.5	9.8	376	S02766	pulmonary surfacta
5	100	9.6	212	I46621	pointerleukin-6
6	100	9.6	212	I46590	interleukin-6 - pi
7	96	9.2	211	ICMS6	interleukin-6 prec
8	91	8.8	211	A34247	interleukin-6 prec
9	86.5	8.3	194	T09255	granulocyte colony
10	85.5	8.3	353	C96711	F24J5.9 (imported)
11	85.5	8.2	2222	A36028	DNA-directed DNA p
12	84.5	8.1	1026	T05882	hypothetical prote
13	84	8.1	212	IVHUB2	
14	83.5	8.0	525	I2BPP5L	Ea59 protein - pha
15	83	8.0	531	C95338	hypothetical Prote
16	82.5	7.9	208	A26496	granulocyte colony
17	82.5	7.9	293	A83055	probable aminacyl
18	82	7.9	492	T22119	hypothetical prote
19	80.5	7.8	960	S44812	F4AB9.6 protein -
20	80	7.7	410	I38502	gene Brn-3b Protei
21	79.5	7.7	6805	S20901	tin - rabbit (fr
22	79	7.6	537	POMVR	gag polypepti
23	79	7.6	925	T29311	hypothetical prote
24	78.5	7.6	207	I46084	interleukin-6 - ca
25	78.5	7.6	530	D96810	hypothetical prote
26	78.5	7.6	797	A3273	cell division prote
27	78	7.5	285	B83588	hypothetical prote
28	78	7.5	404	B71224	hypothetical prote
29	78	7.5	404	A75192	hypothetical prote

ALIGNMENTS

RESULT 1	T09216 interleukin-6 precursor - horse				
C;Species:	Equis caballus (domestic horse)				
C;Date:	11-Jun-1999 #sequence_revision 11-Jun-1999	#text_change 23-Jul-1999			
C;Accession:	T09216				
R;Swiderski, C.B.; Horchov, D.W.					
Submitted to the EMBL Data Library, July 1996					
A;Reference number: 216613					
A;Accession: T09216					
A;Status: Preliminary; translated from GB/EMBL/DDJB					
A;Molecule type: mRNA					
A;Residues: 1-208 <SWI>					
A;Cross-references: EMBL:U64794; NID:92654387; PID:92654388					
C;Genetics:					
C;Keywords: cytokine; growth factor					
Query Match	10.9%	Score 113;	DB 2;	Length 208;	
Best Local Similarity	29.4%	Pred. No. 0.0026;			
Matches 37; Conservatory 22; Mismatches 51; Indels 16; Gaps 5;					
QY 64 ETKNNVPRIOCEDGCDPQLKDNSQFCLQRIOGLAFYKHLID--SDIEKGEPALLPDSP 121					
Db 84 ENNLNPKAEKDCFCQSFSE--NOETCIMKITGGLSERQIYLEYLQEFGKRENKIKTM- 140					
QY 122 MEQLHTSLLGLSQLLQPEDHPRETTQOMPS-----LSSQQWORPLLRSKILRSQAF 173					
Db 141 -QISTKVLL-VQILMQKMKNPNEVTTDPAKSSLAKHSQNEWLNNTTHLILRSLEDF 197					
QY 174 LAIAAR 179					
Db 198 IQLFSLR 203					
RESULT 2	sheep				
C;Species:	Ovis orientalis aries, Ovis ammon aries (domestic sheep)				
C;Date:	10-Sep-1999 #sequence_revision 10-Sep-1999	#text_change 10-Sep-1999			
C;Accession:	S29549				
C;Status: Preliminary					
A;Molecule type: mRNA					
A;Residues: 1-208 <BBR>					
A;Cross-references: EMBL:X68723					
C;Superfamily: interleukin-6					
R;Ebrahimi, B.					
Submitted to the EMBL Data Library, October 1992					
A;Reference number: S29549					

Query Match 10.6%; Score 110; DB 1; Length 208;
 Best Local Similarity 25.5%; Pred. No. 0.0051; Gaps 8;
 Matches 51; Conservative 27; Mismatches 84; Indels 38; Gaps 8;

Qy 8 IMIWLLPWTQGLAVPRSSSPDWAQCQLSRLNCLMIAWNAAHAPAGH---MNLRR---E 59
 Db 14 VSLPLLVMVTSAAFTPQGFLKNDTPPSLLLTPEKTEALKHIVDKISAIKEICE 73

Qy 60 EDEE----ETKNNVPRIQCEQCDPGLKNSQFCLQRIOGLAYKHLID--SD 108
 Db 74 KNDCENSKETLAENKLKPLMEERKGCFQSGF--NOAVCLIKTAGLLEYQIVYIQLDFQN 131

Qy 109 IFKGEPAALLPDSPMEQLHTSLIGLSQLQ-----DPHPRETOQMPSSLSQQWQR 159
 Db 132 EFGSN---QEVVMELOSSRTLTIKERKINGLITPATH--TDLEKMQSSNEWVK 183

Qy 160 PLRSKILRSQAFALATAAR 179
 Db 184 NAKVIIILRSLENFQPLRL 203

RESULT 3
 A56610 interleukin-6 precursor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A56610; S22162
 R;Broograms, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
 DNA Seq. 2, 411-413, 1992
 A;Title: Nucleotide sequence of bovine interleukin-6 cDNA.
 A;Reference number: A56610; PMID:1446077
 A;Accession: A56610
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-208 <DRO>
 A;Cross references: EMBL:X57317; NID:92193; PID:CAA40572.1; PID:92194
 A;Experimental source: BLV induced B cell-lymphosarcoma
 A;Note: sequence extracted from NCBI backbone (NCBIP:118917)
 C;Superfamily: interleukin-6
 C;Keywords: cytokine

Query Match 10.0%; Score 104; DB 1; Length 208;
 Best Local Similarity 26.8%; Pred. No. 0.019; Gaps 5;
 Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;

Qy 59 EEEDE----ETKNNVPRIQCEQCDPGLKNSQFCLQRIOGLAYKHLID--S 107
 Db 73 EKNDECESSSETLAENKLKPLMEERKGCFQSGF--NOAVCLIRTTAGLLEYQIVYIQL 130

Qy 108 DIFGEPAALLPDSPMEQLHTSLIGLSQLQPE-----DPHPRETOQMPSSLSQQWQRPL 161
 Db 131 NEYEGNQENVRD----ERKNIKRTLQILKQTAIDLITTPATNDLLEKMQSSNEWVKNA 185

Qy 162 LRSKILRSQAFALATAAR 179
 Db 186 KITILRNLFNQFSLR 203

RESULT 4
 S02766 pulmonary surfactant protein B precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: S02766
 R;Emrie, P.A.; Shannon, J.M.; Mason, R.J.; Fisher, J.H.
 Biochim. Biophys. Acta 994, 215-221, 1989
 A;Title: cDNA and deduced amino acid sequence for the rat hydrophobic pulmonary surfactant
 A;Reference number: S02766; PMID:89150284
 A;Accession: S02766
 A;Molecule type: mRNA
 A;Residues: 1-376 <MR>
 A;Cross-references: EMBL:X147284; PID:957285
 C;Superfamily: pulmonary surfactant protein B; saposin repeat homology

Query Match 9.8%; Score 101.5; DB 2; Length 376;
 Best Local Similarity 29.3%; Pred. No. 0.068;
 Matches 55; Conservative 22; Mismatches 70; Indels 41; Gaps 11;

Qy 10 LWLIPFW-TGOLAVPRSSSPDWQ-----CQOLSRNL----CMIAWNAAHAPASHM-- 54
 Db 9 LLPLPTLCSLGAATESASSSPDCAGPKFWCQSLEQATQCRALGHQLOEWVGHAGANDLCQ 68

Qy 55 -----NLREEDDEETRNVPRIQCEQCDPGLKNSQFCLQRIOGLAYKHLIDSD 108
 Db 69 ECEDIVHLTKMTKEDAFQDTIKFLBEDCIDLPLK---LIVPQRQVLDVYLPLV-ID 123

Qy 109 IFKGEPAALLPDSPMEQLHTSLIGLSQLQPEDHPRETOQMPSSLSQQWQRPLRSKILR 168
 Db 124 YFGQG--IKPKAICS--HVGLCPLGQ-TKPEQKPEMLAIPN-----PLLNKLVLP 169

Qy 169 SLO-AFLA 175
 Db 170 ALPGAFIA 177

RESULT 5
 I46621 prointerleukin 6 - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Accession: I46621
 R;Richards, C.; Saklatava, J.
 Cytokine 3, 265-276, 1991
 A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression
 A;Reference number: MUID:91338547; PMID:1873476
 A;Accession: I46621
 A;Molecule type: mRNA
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Cross-references: GB:M86722; NID:9164624; PIDN: AAC37333.1; PID:g164625
 A;Genes: IL6
 C;Superfamily: Interleukin-6

Query Match 9.6%; Score 100; DB 2; Length 212;
 Best Local Similarity 25.0%; Pred. No. 0.047;
 Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps

Qy 52 GHMLLREEDE-----ETKNNVPRIQCEQCDPGLKNSQFCLQRIOGL 98
 Db 62 GKISAMRKEMCEKEYKECENSKEVLAENNINLPKAEDQCFQSF--NOETCLMRITTG 119

Qy 99 AFYKHLID---SDIFKGEPAALLPDSPMEQLHTSLIGLSQLQPEDHPRETOQMPSS 150
 Db 120 VEFQIYDLYKEYESNKG-----YEAOVISTKALIQTLEQKGKNPDRATTPNPTT 171

Qy 151 -----LSSSQWQPLRSKILRSQAFALATAAR 179
 Db 172 NAGLLDKLQSONEWMMKNTKILILRSLEDFLQFSLR 207

RESULT 6
 I46590 interleukin 6 - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Accession: I46590
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 R;Mathalagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A;Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation co

A; Reference number: I46590; MUID:92360284; PMID:1497880
 A; Accession: I46590
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 B; Residues: 1-211 <PATN>
 A; Cross-references: GB:M80258; NID:9164514; PIDN: AAC27127.1; PID:9164515
 C; Genetics:
 B; Gene: IL-6
 C; Superfamily: interleukin-6
 Query Match 9.6%; Score 100; DB 2; Length 212;
 Best Local Similarity 25.0%; Pred. No. 0.047; Indels 38; Gaps 5;
 Matches 39; Conservative 22; Mismatches 57; A; Cross-references: GB:M80258; NID:9164514; PIDN: AAC27127.1; PID:9164515
 A; Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleav
 A; Reference number: A90157; MUID:9014791; PMID:2302197
 A; Molecule type: protein
 A; Molecular type: protein
 A; Residues: 66-69; X⁷¹-75-78-94-128-148 <JAS>
 R; Van Snick, J.; Cyphas, S.; Vink, A.; Oyttenhove, C.; Coulie, P.G.; Rubira, M.R.; S
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A; Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lympho
 A; Reference number: A26662; MUID:8709211; PMID:2948184
 A; Accession: A26662
 A; Molecule type: protein
 A; Residues: 25-39; X⁴¹-42-X⁴⁴-45 <VSNS>
 R; Chiu, C.-P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A; Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA C
 A; Reference number: A40486; MUID:8901745; PMID:3262872
 A; Accession: A40486
 A; Molecule type: mRNA
 A; Residues: 1-211 <CHI>
 A; Cross-references: GB:J03783; NID:9198367; PIDN:AAA39301.1; PID:9309410
 R; Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.
 Blood 72, 2070-2073, 1988
 A; Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleuki
 A; Reference number: A60799; MUID:89062753; PMID:326198
 A; Accession: A60799
 A; Molecule type: protein
 A; Residues: 77-98 <SHA>
 R; Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A; Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a
 A; Reference number: S10241; MUID:90171860; PMID:2106569
 A; Accession: S10241
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-6 <BLA>
 A; Accession: A60799
 R; Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A; Title: Specific covalent modification of the tryptophan residues in murine interleu
 R; Tanabe, O.; Akira, S.; Szikora, J.P.; Renaud, J.C.; van Roost, E.; Boon, T.; Shim
 J. Immunol. 141, 3875-3881, 1988
 A; Title: Genomic structure of the murine IL-6 gene. High degree conservation of potentia
 A; Reference number: A30331; MUID:89035525; PMID:3263439
 A; Accession: A30331
 A; Molecule type: DNA
 A; Residues: 1-211 <PATN>
 A; Cross-references: GB:M20572; NID:9198369; PIDN:AAA39302.1; PID:9387386
 R; Van Snick, J.; Cyphas, S.; Szikora, J.P.; Renaud, J.C.; van Roost, E.; Boon, T.; Shim
 Eur. J. Immunol. 18, 193-197, 1988
 A; Title: cDNA cloning of murine interleukin-HP1, homology with human interleukin 6.
 A; Reference number: A27610; MUID:88166883; PMID:2965020
 A; Accession: A27610
 A; Molecule type: mRNA
 A; Residues 1-211 <AN>
 A; Cross-references: GB:X06203; NID:952701; PID:952702
 R; Mock, B.R.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cle
 J. Immunol. 142, 1372-1376, 1989
 A; Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
 A; Reference number: A30571; MUID:89124383; PMID:2566387
 A; Accession: A30571
 A; Molecule type: mRNA
 A; Residues 5-211 <HOC>
 A; Cross-references: GB:W24221; NID:9341131; PIDN:AA68814.1; PID:9870659
 R; Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 18-19, 1988
 A; Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and r
 A; Reference number: S01323; MUID:88329059; PMID:3262059
 A; Accession: S01323
 A; Molecule type: protein
 A; Residues 25-166' X¹⁶⁸-211 <SIMP>
 A; Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 R; Grenett, H.E.; Fuentes, N.B.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A; Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 A; Accession: S12103; MUID:9105159; PMID:2243807
 A; Molecule type: mRNA

A; Status: translated from GB/EMBL/DDJB	
A; Molecule type: protein	
A; Residues: 1-212 <BRA>	
A; Cross-references: GB: M18403; NID: g184631; PID: AAA52729.1; MUID: 9306911	
A; Content: Produced by both lymphoid and nonlymphoid tissue in response to growth factor secretion. It therefore appears to function as an autoregulator of cell growth.	
C; Comment: This protein plays a regulatory role in various host defense mechanisms.	
C; Genetics:	
A; Gene: GDB: IL6	
A; Cross-references: GDB: 120748; OMIM: 147620	
A; Map Position: 7p21-7p21	
A; Introns: 7/1; 70/3; 108/3; 157/3	
C; Superfamily: interleukin-6	
C; Keywords: Castelman's disease; cytokine; extracellular protein; glycoprotein; growth factor; interleukin-6	
F; 1-27/Domain: signal sequence #status predicted <SIG>	
F; 28-121/Product: interleukin-6, long form #status experimental <MATL>	
F; 28-122/Product: interleukin-6, short form #status experimental <MAT5>	
F; 30-112/Product: interleukin-6, short form #status experimental	
F; 72-78, 101-111/Disulfide bonds: #status experimental	
F; 73-79/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental	
F; 166/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental	
F; 172/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match Score: 8.18; DB 1; Length 212;	
Best Local Similarity: 21.5%; Pred. No. 1.5;	
Matches 38; Conservative 28; Mismatches 71; Indels 40; Gaps 7;	
Qy 15 WWTGQAVPRASSPPDWAQQQLSRMCLAWNAAHAPGMNLLREPEEDETKANVPRIQC 74	
Db 59 YILDGISALRKET----CNK-SMCCESSKEALA-----ENNLNLPKAE 97	
Qy 75 EDGCDPGLDKNDSQFLQRIGQLAGFYKHLD--SDIFKGEPALLPDSPMEQLITSLGL 132	
Db 98 RDGCFOSGF--NEETCLVK ITGLIEEVLEYLNRFESS---EEGARAYQMSTKVL 150	
Qy 133 SQLQPE-----DHPRETQQMPSSLSQQWORPLIIRSKLRSQAFALTAAR 179	
Db 151 IQLFLQRKAKNLDAITTPDPTTNASILTKLQAQNWLQDMTTHLIRSFKEFLQSSLR 207	
RESULT 14	
ZEBP5L	
E559 protein - phage lambda	
C: species: Phage lambda	
C: Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999	
R: Daniels, D.	
A: Reference number: A94614	
A: Accession: D43009; PMID: A04379	
A: Accession: D43015; PMID: A04379	
A: Accession: D43015	
A: Molecule type: DNA	
A: Residues: 1-525 <DAN>	
R: Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.	
J. Mol. Biol. 162: 729-773, 1982	
A: Title: Submitted to the Nucleic Acid Sequence Database, September 1982	
A: Reference number: A94614	
A: Accession: D43009	
A: Molecule type: DNA	
A: Residues: 1-525 <SAN>	
R: Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.	
J. Mol. Biol. 162: 729-773, 1982	
A: Title: Nucleotide sequence of bacteriophage lambda DNA.	
A: Reference number: A92891; PMID: 83189071; PMID: 6221115	
A: Accession: D43015	
A: Molecule type: DNA	
A: Residues: 1-525 <SAN>	
A: Cross-references: GB: J02459; PMID: 921510	
C: Genetics:	
A: Gene: Eα59	
A: Accession: 55-61-52-37	
C: Superfamily: phage lambda Eα59 protein	
Query Match Score: 8.08; DB 1; Length 525;	
Best Local Similarity: 27.8%; Pred. No. 5.3;	
Matches 40; Conservative 15; Mismatches 62; Indels 27; Gaps 6;	
Qy 63 EETKNNVPRIQCQGDQGLKDNSQFCLQRIGQLAGFYKHLD--DIRKGEPALLPD5 120	
Db 333 EELRNEFQIQYDDKTFKLFDNTQKYLMMSSGHAVLFITLVYGEKSLYLFDE 392	
Qy 121 PMEQLHTSLLG----LSQLOPED-----HPTQMQPSLSSQQWORPLRSKIL 167	
Db 393 PEVHLHPPLLSAFLTSLDLDLARGVALLYATHSPVVLQEV----RSCMW----KVL 442	
A: Title: Disulfide structures of human interleukin-6 are similar to those of human granulocyte interleukin-6.	
A: Reference number: S04981; PMID: 89286115; PMID: 272117	
A: Content: annotation; disulfide bonds in recombinant protein	
R: Rock, P.L.; Li, X.; Chong, P.; Iida, N.; Klein, M.	
Biochemistry 37: 5146-5154, 1994	
A: Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.	

Qy 168 RSLQAFLLAIAARV--FAHGAATLTI 189
 || :|| | :| :|
 Db 443 FSRREATNITRDPIEFGENIGVLT 466

RESULT 15

C95338 Hypothetical protein Smal131 [Imported] - Sinorhizobium meliloti (strain 1021) magaplasm

C.Species: Sinorhizobium meliloti

C.Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C.Accession: C95338

Rj.Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows ; Kaiman, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A.Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A;Reference number: A95262; MUID:21396509; PMID:11481432

A.Accession: C95338

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-531 <UR>

A;Cross references: GB:AB006469; PIDN:IAK65369_1; PID:g14523721; GSPDB:GN00165

Rj.Experiment: source: strain 1021, megaplasmid pSymA

Rj.Author: Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Barloy-Hubler, F.; Fedderspiel, N.A.; Fisher, R.F.;

peila, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Lelauze, K.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keeting, D.H.; Kiss, E.; Komp, C.; Lelauze,

hebault, P.; Vandembel, M.; Vorhofer, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Contents: reference number: A96039; MUID:21368234; PMID:11474104

C;Contents: annotation

C;Genetics:

A;Gene: Smal131

A;Genome: plasmid

Query	Match	Score	Length
Qy	8.0%	531;	
Best Local Similarity	21.7%	Pred. No. 6;	
Matches	33;	Mismatches	24;
		Indels	Gaps 5;

Query	Match	Score	Length
Qy	8.0%	531;	
Best Local Similarity	21.7%	Pred. No. 6;	
Matches	33;	Mismatches	24;
		Indels	Gaps 5;

Db 198 LLQEDAKAPS6WDYVICESTIYGNIEREADDAARRHLSEVLTAAIPNGALLIPSFAVE 257

Qy 93 RIRQGLAFYKHLLSD1FKGPALLPDSPMELQLHTSLLGSQLQPEDHPRTIQOMPSL- 151

Db 258 RQELLTDLVHIMETAVPKCPII-DSPATRASEIF----RRHARELENGDALV 308

Qy 152 ---SSSQWQRPLRSKILRSQAF-LATAA 178

Db 309 RGIESKNVRFETAEOSKAVDLDLRFHIVTA 340

Search completed: November 20, 2002, 11:55:02

Job time : 16.7636 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	115	11.1	208	1	IL6_SHEEP	P29455 ovis aries
2	113	10.9	208	1	IL6_HORSE	Q95181 equus cabal
3	110	10.6	208	1	IL6_CAPIRI	Q28319 capra hircu
4	106.5	10.3	205	1	IL6_ORCOR	Q28747 orcinus orc
5	104	10.0	208	1	IL6_BOVIN	P26892 bos taurus
6	103	9.9	208	1	IL6_FELCA	P41683 felis silve
7	101.5	9.8	376	1	PSPB_RAT	P22355 rattus norv
8	100	9.6	212	1	IL6_TIG	P26893 sus scrofa
9	97	9.3	207	1	IL6_CANFA	P41323 canis famil
10	96	9.2	211	1	IL6_MOUSE	P08505 mus musculu
11	91	8.8	211	1	IL6_RAT	P20607 rattus norv
12	90	8.7	209	1	IL6_PHOVI	Q28819 phoca vitul
13	89.5	8.6	525	1	VE59_LAMBD	Q77438 drosophila
14	89	8.6	457	1	NH20_CAELF	Q9565 caenorhabdi
15	86.5	8.3	194	1	CSF3_FELCA	Q02708 felis silve
16	86.5	8.3	195	1	CSF3_PIG	P02837 sus scrofa
17	85.5	8.2	222	1	DPOE_YEAST	P21951 saccharomyces
18	84	8.1	212	1	IL6_HUMAN	P05231 homo sapien
19	83.5	8.0	525	1	VFR3_DROME	P03754 bacterioph
20	82.5	7.9	208	1	CSF3_MOUSE	P09920 mus musculu
21	82.5	7.9	212	1	IL6_CERTO	P46650 cercopithecus
22	82	7.9	710	1	ABBI_HUMAN	Q00213 homo sapien
23	81.5	7.9	175	1	CSF3_CANFRA	P35834 canis famil
24	80.5	7.8	207	1	IL6_NARMO	Q35736 marmota mon
25	80.5	7.8	207	1	IL6_HUMSVI	P34427 caenorhabdi
26	80	7.7	212	1	LI36_CAEEL	P79341 macaca fasc
27	80	7.7	410	1	BR3B_HUMAN	Q12837 homo sapien
28	80	7.7	708	1	ABBI_MOUSE	Q99xj1 mus musculu
29	79	7.6	537	1	GAG_MLYRD	P11269 radiation m
30	78.5	7.6	125	1	IL6_MACMUI	P41693 mustela vis
31	78.5	7.6	222	1	COLJ_CYPICA	Q9YK5 c corticot
32	78	7.5	212	1	IL6_MACMU	P51494 macaca mulu
33	77.5	7.5	513	1	ACHD_CHICK	P02717 gallus gall

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40:
Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
ID _IL6_SHEEP STANDARD; PRT; 208 AA.
AC P29455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS ovis aries (Sheep).
OU Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:94041419; PubMed:8225400;
RA Andrews A.E., Barcham G.J., Asman K., Meeußen E.N.T., Brandon M.R., Nash A.D.; RT "Molecular cloning and characterization of a ruminant interleukin-6 CDNA." RT Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ebrahimi B.
RL Submitted (Oct-1992) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

DR InterPro: IPB03573; IL6_MGF_GCF. DR InterPro: IPB03574; Interleukin_6. DR EMBL: X62501; CAA44363_1; DR EMBL: X68723; CAA88662_1; DR PRIM: A19159; CAA01443_1; DR PIR: S29549; S29549. DR HSSP: P05231; IL6. DR InterPro: IPB03573; IL6_MGF_GCF. DR InterPro: IPB03574; Interleukin_6. DR Pfam: PF0088; IL6; 1. DR PRINTS: PR00433; IL6GCSFMGF. DR PRODOM: PD004356; Interleukin_6; 1. DR SMART: SM0126; IL6; 1. DR PROSITE: PS00254; INTERLEUKIN_6; 1. DR Cytokine; Glycoprotein; Growth factor; Signal. KW SIGNAL 1 29 BY SIMILARITY.

FT	CHAIN	30	208	INTERLEUKIN-6.	DR	EMBL; U64794; AAB87703; 1; -.
FT	DISULFID	72	78	BY SIMILARITY.	DR	EMBL; AF005227; AAB6224; 1; -.
FT	CARBOYD	101	111	BY SIMILARITY.	DR	EMBL; AF041375; AAC04574; 1; -.
FT	CONFLICT	38	38	N-LINKED (GLCNAC. . .) (POTENTIAL).	DR	HSSP; P05231; IAU03.
FT	CONFLICT	4	4	L -> R (IN REF. 2).	DR	InterPro; IPR003573; IL6_MGF_GCSF.
FT	CONFLICT	110	110	I -> V (IN REF.).	DR	InterPro; IPR003574; Interleukin_6.
FT	CONFLICT	171	171	M -> L (IN REF.).	DR	Pfam; PF0489; IL6; 1.
FT	CONFLICT	201	201	S -> R (IN REF.).	DR	PRINTS; PRO0433; IL6csMF.
SO	SEQUENCE	208 AA:	23446 MW:	EBC96C13E3230A CRC64;	DR	PRODOM; PD004356; Interleukin_6; 1.
Query Match		11.18;	Score 115;	DB 1; Length 208;	DR	SMART; SM00126; IL6; 1.
Best Local Similarity		25.58;	Pred. No. 0.00059;	Gaps 8;	DR	PROSITE; PS00254; INTERLEUKIN_6; 1.
Matches 51;	Conservative	28;	Mismatches 83;	Indels 38;	KW	Cytokine; Glycoprotein; Growth factor; signal.
Qy	8	IMMWLFWVTSGLAVPRSSSDWAQQQLSRNLCLMWNHAPASH-	~MNLRL--E	59	FT	POTENTIAL.
Db	14	VSGULLVMTSAFPTGPGDFKDNTTPSRLLTPEKTEALKHIVDKISATRKETICE	73		FT	INTERLEUKIN-6.
Qy	60	EEDE-----ETKRNVPIQDGGCDPGLKDNQSFCFLQRFRGLAFYKHLD--SD	108		FT	BY SIMILARITY.
Db	74	RIDECENSKEDLAENKLKPLMEERDQGCQSGF--NQATCILIKTAGLLEYQIVLDFLON	131		FT	DISULFID
Qy	109	IFKGEPAALLPPSPMEQLTSLIGLSQLQ-----PDDHPRETOQMFESLSSQQMQR	159		FT	98
Db	132	EFGN----QETVMELOSSRTLQIQLKEIAGLITTPATH--TDMLEKMOSSNEWVK	183		FT	108
Qy	160	PFLRSKILRSQAFALATAAR	179		FT	108
Db	184	NARYVIIILRSLENFLQFSLR	203		FT	108
<hr/>						
RESULT 2				Query Match	10.9%; Score 113;	DB 1; Length 208;
ID	IL6_HORSE	STANDARD;	PRT;	Best Local Similarity	29.4%; Pred. No. 0.00092;	Gaps 5;
AC	Q51818;	019007; 046568;	AA.	Matches 37;	Conservative 22;	Mismatches 51;
DT	01-NOV-1997	(Rel. 35; Created)		FT	Indels 16;	Gaps
DT	15-JUL-1999	(Rel. 38; Last sequence update)		FT		
DT	15-JUN-2002	(Rel. 41; Last annotation update)		FT		
DE	Interleukin-6 precursor (IL-6).			FT		
GN	IL6.			FT		
OS	Equus caballus (Horse).			FT		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			FT		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			FT		
OX				FT		
RN	[1]			FT		
RP	SEQUENCE FROM N.A.			FT		
RA	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			FT		
RL	[2]			FT		
RN	SEQUENCE FROM N.A.			FT		
RA	Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;			FT		
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			FT		
RN	[3]			FT		
RP	SEQUENCE FROM N.A.			FT		
RA	Lai A.C.K.;			FT		
RL	"Cloning and expression of equine interleukin-6."			FT		
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases			FT		
CC	-!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS; IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).			FT		
CC	-!- SUBCELLULAR LOCATION: Secreted.			FT		
CC	-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			FT		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			FT		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			FT		
CC	SEQUENCE FROM N.A.			FT		
RP	SEQUENCE FROM N.A.			FT		
RA	Takakura H., Mori Y., Tatsumi M.			FT		
RA	"Molecular cloning of caprine IL-6 cDNA and its expression in insect cells."			FT		
RL	Int. Arch. Allergy Immunol. 113:409-416(1997).			FT		
CC	-!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS; IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.			FT		
CC	-!- SUBCELLULAR LOCATION: Secreted.			FT		
CC	-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			FT		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			FT		
CC	SEQUENCE FROM N.A.			FT		
RP	SEQUENCE FROM N.A.			FT		
RA	Takakura H., Mori Y., Tatsumi M.			FT		
RA	"Molecular cloning of caprine IL-6 cDNA and its expression in insect cells."			FT		
RL	Int. Arch. Allergy Immunol. 113:409-416(1997).			FT		
CC	-!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS; IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.			FT		
CC	-!- SUBCELLULAR LOCATION: Secreted.			FT		
CC	-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			FT		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).			FT		

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; D88569; BA13118.1; -.

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR InterPro; IPR003574; Interleukin_6.

DR Pfam; PF0489; IL6_1.

DR PRINTS; PR00433; TI6GCSPEMGF.

DR Prodrom; PD004356; Interleukin_6; 1.

DR SMART; SM00126; IL6_1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 29 BY SIMILARITY.

FT CHAIN 30 208 INTERLEUKIN_6.

FT DISULFID 72 78 BY SIMILARITY.

FT DISULFID 101 111 BY SIMILARITY.

FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQ SEQUENCE 208 AA; 23423 MW; E92E0BF3E3230A CRC64;

Query Match 8 IMIWLLPPVYTOGLAVPRSSSPDIAQCOOLSRNCMLAWNAAAPAGH---MNNLR---E 59

Best Local Similarity 10.6%; Score 110; DB 1; Length 208;

Matches 49; Conservative 29; Mismatches 87; Indels 32; Gaps 7;

Db 14 VSLGLLYMTSAAPTGPGLGEKFNDTPSRLIITTPKETEALIHKIVDTKSARKEICE 73

QY 60 EDEE----- ETKNNVPRQCEDGDPQLKDNQSFCQLRIGAFYKLHD--SD 108

Db 74 KNDCENSKETLAENKLKLPKEEKDGCFCQSEF--NQAICLKTAGLLEYQTYLDFLQN 131

QY 109 RPKGEPALPDSEMEQLTISLQLSQILOPE----DHPRETOOMPSSLSSQQMORPLL 162

Db 132 EFGN----QEVYMELOSSRTLQIILKEKFLAGLITTPATNTDMLEKMOSSNEWVNAK 186

QY 163 RSKLRLSQAQFLAIAR 179

Db 187 VILLRSLENFLQFSLR 203

RESULT 4

IL6_ORCOR ID IL6_ORCOR STANDARD; PRT; 205 AA.

AC Q28147; DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE Interleukin-6 precursor (IL-6) (Fragment).

GN IL6.

OS Orcinus orca (Killer whale).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus.

NCBI_TAXID=9733;

RN [1]

RX MEDLINE=96163018; PubMed=8575817;

RA King D.P.; Schrenzel M.D.; McKnight M.L.; Reidarson T.H.; Hanni K.D.; RA Scott J.L.; Ferrick D.A.;

RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from the harbor seal (*Phoca vitulina*), killer whale (*Orcinus orca*), and Southern sea otter (*Enhydra lutris nereis*).";

RU Immunogenetics 43:190-195(1996).;

CC FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).

CC SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

CC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC

DR EMBL; L46803; ARB01429.1; -.

DR HSSP; P05231; IALU.

DR InterPro; IPR003573; IL6_MGF_GCSF.

DR InterPro; IPR003574; Interleukin_6.

DR Pfam; PE00489; IL6_1.

DR PRINTS; PR00433; TI6GCSPEMGF.

DR Prodrom; PD004356; Interleukin_6; 1.

DR SMART; SM00126; IL6_1.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT NON-TER 1 1 BY SIMILARITY.

FT SIGNAL <1 21 BY SIMILARITY.

FT CHAIN 22 205 INTERLEUKIN_6.

FT DISULFID 64 70 BY SIMILARITY.

FT DISULFID 93 103 BY SIMILARITY.

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 205 AA; 23266 MW; 6308F3A57966832 CRC64;

Query Match 10.3%; Score 106.5; DB 1; Length 205;

Best Local Similarity 27.3%; Pred. No. 0.0038;

Matches 42; Conservative 25; Mismatches 54; Indels 33; Gaps 7;

QY 52 GHMNLREDEE-----ETKNNVPRQCEDCDPQQLKDNQSFCQLRIGOL 98

Db 54 GKISAMRKENCEKVDKCENSKEAENNLNPKMAEKDCFCQSGF--NQETCLMRITGL 111

QY 99 AFYKHLDD--SDIFGGEPAALLPDSPMEQLHTSLLGSQULL-QPEDHPRE-TQOMPSSLSS 154

Db 112 LEYQIYDYLQNEYEGD----KEAIEAVQISSKALAQILRKVKNPDEVTDPPTINAS 166

QY 155 -----QOWQPPLRSRSLRSQIAFLAIAR 179

Db 167 LMNNLQSQNDWMKNTKILILRSLENFLQFSLR 200

RESULT 5

IL6_BOVIN ID IL6_BOVIN STANDARD; PRT; 208 AA.

AC P26892; DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-6 precursor (IL-6).

GN IL6.

OS Bos taurus (Bovine).

OS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OC NCBITaxonID=9913;

RN [1]

RX SEQUENCE FROM N.A.

RC STRAIN-Holstein;

RC MEDLINE=3076003; PubMed=1446077;

RA Drogemans L., Cluets I., Cleuter Y., Kettmann R., Burny A.;

RT "Nucleotide sequence of bovine interleukin-6 cDNA.";

RL DNA Seq. 2:411-413(1992).

CC FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; X57317; CAA40572.1; .
 DR PIR; S22162; S22162.
 DR HSPP05231; 1116.
 DR InterPro; IPR003573; IL6_MGE_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00485; IL6; 1.
 DR PRNTS; PRO00433; IL6GSEFMGF.
 DR PRODOM; PD0004356; Interleukin_6; 1.
 DR SMART; SM00116; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR CYTOKINE; Glycoprotein; Growth factor; Signal.
 KW SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 208 INTERLEUKIN-6.
 FT DISULFID 72 78 BY SIMILARITY.
 FT DISULFID 101 111 BY SIMILARITY.
 CARBOHYD 38 38 N-LINKED (GLCNAC, .) (POTENTIAL)
 SEQUENCE 208 AA; 23758 MW; A0F000B9BA2EC341 CRC64;
 Query Match 10.0%; Score 104; DB 1; Length 208;
 Best Local Similarity 26.8%; Pred. No. 0.0067;
 Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;
 Qy 59 FEEDS-----ETRNINPRIQCEGCDFOGLKNSQFLQRQGAFYKHLID-S 107
 Db 73 EKNDCESSKETLAENKUNLPKMEKDGCFCQSGF--NOAQLIRTAGLLEYQIYLDLQ 130
 Qy 108 DIFKGEPALLPDSPMEOQHTSLIGLSQOLQPE-----DHPRETOQMPSSQQWQPL 161
 Db 131 NEYGNQNENVRD-----LTKNTRPLIQIKORIADLTTPNTDLERAMOSSNEWVKA 185
 Qy 162 LRSKLRLSQAQFLAIAAR 179
 Db 186 KIILRLNENFLQSLR 203

RESULT 6

	IL6_FELCA	STANDARD;	PRT;	208 AA.
ID	IL6_FELCA			
AC	P41633;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-6 precursor (IL-6).			
GN	IL6			
OS	<i>Felis silvestris catus</i> (Cat).			
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI-TAXID=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94162386; PubMed=8117820;			
RX	Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H., Hasewawa A.; Molecular cloning of feline interleukin-6 cDNA.";			
RT	"Molecular cloning of feline interleukin-6 CDNA.";			
J. Vet. Med. Sci.	55:941-944 (1995).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RX	TISSUE=Lymphocytes;			
RX	RC MEDLINE=94052249; PubMed=8234373;			
RA	Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;			
RT	"Molecular cloning and characterization of a cDNA encoding feline interleukin-6.";			
RT	Proc. Soc. Exp. Biol. Med. 204:301-305(1993).			
CC	"FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION			

CC	OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC	- 1 - SUBCELLULAR LOCATION: Secreted.
CC	- 1 - SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC	EMBL; D16914; AAA16620_1; .
DR	EMBL; D13227; BRA02507_1; .
DR	HSSP; P05231; IL16.
DR	InterPro; IPR003573; IL6_MGE_GCSF.
DR	InterPro; IPR003574; Interleukin_6.
DR	Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSMCF.	
DR	PRODOM; PD004356; Interleukin_6; 1.
DR	SMART; SM00126; IL6; 1.
DR	PROSITE; PS00254; INNERLEUKIN_6; 1.
RW	CYCOKINE; Glycoprotein; Growth factor; Signal.
FT	SIGNAL 1 27 POTENTIAL.
FT	CHAIN 28 208 INTERLEUKIN_6.
FT	DISULFID 68 74 BY SIMILARITY.
FT	DISULFID 97 107 BY SIMILARITY.
FT	CONFLICT 2 2 T -> N (IN REF. 2).
FT	CONFLICT 45 45 S -> P (IN REF. 2).
FT	CONFLICT 133 133 E -> K (IN REF. 2).
FT	CONFLICT 173 187 AKLSHRRVVAHHNN (IN REF. 2).
FT	CONFLICT 200 201 FS -> LR (IN REF. 2).
SEQUENCE	208 AA; 23401 MW; 93B4456B2989CA4C CRC64;
QY	Query Match 9.9% Score 103; DB:1; Length 208;
Best Local Similarity 24.8%; Pred. No. 0.0083;	
Matches 38; Conservative 28; Mismatches 55; Indels 32; Gap 1	
QY	52 GHNLRLRE-----EDE-----ETKNNVPRIQEDGCDPQLKDNSQFCQLQRIGQL 9
Db	58 GKTALKKEMCNYNRCEDSKTALAENLNULPKLAEKDGCFQSGF -NOETCLTRTTGL 1
QY	99 AFYKHLD--SDIFKGEPALLDSPMEQLITSLGGSQLLOPDHRETQOMP----- 1
Db	116 QEQIYKLFLQDKYEGD----EENAKSVITSTNVLLQMKRKGKNDDEVTFPVPTVEVG 1
QY	150 -- SLSSSQWQRPLRFLRSKILNLSLQATLALAR 179
Db	171 LQAKLQSQEWWLRHTTITHLTLRRLDEDLFQFSLR 203
RESULT 7	PPSPB_RAT STANDARD; PRT; 376 AA.
ID	PPSPB_RAT
AC	P2255;
DT	01-AUG-1991 (Rel. 19, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Pulmonary surfactant-associated protein B precursor (SP-B) (Pulmonary surfactant-associated proteolipid SPc(Phe)).
GN	SFTPB OR SFTB3.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus
OC	NCB_TaxID=10116;
OX	[1]
RP	SEQUENCE FROM N A.
RX	MEDLINE=9150248; PubMed=2920185;
RA	Emrie P.A.; Shannon J.M.; Mason R.J.; Fisher J.H.;
"	"cDNA and deduced amino acid sequence for the rat hydrophobic

RT pulmonary surfactant-associated protein, SP-B, ";

RL Biochim. Biophys. Acta 994:215-221(1989).

CC -!- FUNCTION: PULMONARY SURFACTANT-ASSOCIATED PROTEINS PROMOTE ALVEOLAR STABILITY BY LOWERING THE SURFACE TENSION AT THE AIR-CC LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES. SP-B INCREASES THE COLLAPSE PRESSURE OF PALMITIC ACID TO NEARLY 70 MILLINEWTONS

CC PER METER.

CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

CC -!- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, 2 CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

CC -!- SIMILARITY: CONTAINS 1 Saposin A-type DOMAIN.

CC -!- SIMILARITY: CONTAINS 3 Saposin B-type DOMAINS.

CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL: X14778; CAA32885.1; - .

CC DR PIR: S02766; S0766.

CC DR HSSP: P07988; 1DFW.

CC DR InterPro: IPR003119; SapA.

CC DR InterPro: IPR000004; SapB.

CC DR Pfam: PF002199; SapA; 1.

CC DR Pfam: PF03489; Surfactant_B; 1.

CC DR ProDom: PD001732; SapB; 1.

CC DR SMART; SM00162; SAPA; 1.

CC DR SMART; SM00118; SAPB; 3.

CC KW Surface film; Gaseous exchange; Glycoprotein; Repeat.

CC FT PROPEP 1 190

CC FT CHAIN 191 269

CC FT PROPEP 270 376

CC FT DOMAIN 26 59

CC FT DISULFID 198 267

CC FT DISULFID 201 261

CC FT DISULFID 225 236

CC FT DISULFID 238 238

CC FT CARBOHYD 306 306

CC SEQUENCE 376 AA: 41590 MW; F329DC62E733FB4C CRC64;

FT B.

FT PROPEP 9.8%; Score 101.5; DB 1; Length 376;

FT DOMAIN 29.3%; Pred. No. 0.024;

FT Matches 55; Conservative 22; Mismatches 70; Indels 41; Gaps 11;

FT FT SAPOSIN-LIKE TYPE A.

FT FT BY SIMILARITY.

FT FT BY SIMILARITY.

FT FT BY SIMILARITY.

FT FT BY SIMILARITY.

FT FT INTERCHAIN (BY SIMILARITY).

FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT FT PROTEIN: PS00254; INTERLEUKIN_6; 1.

FT FT CYTOKINE; Glycoprotein; Growth factor; Signal.

FT FT SIGNAL 1 29 BY SIMILARITY.

FT FT CHAIN 30 212 BY SIMILARITY.

FT FT DISULFID 72 78 BY SIMILARITY.

FT FT DISULFID 101 111 BY SIMILARITY.

FT FT CONFLICT 30 30 E -> G (IN REF. 1).

FT FT SEQUENCE 212 AA; 23952 MW; 1E736FB230BA4FC5D CRC64;

Query Match 9.6%; Score 100; DB 1; Length 212;

Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps 5;

QY 10 LLILPPW-TQGLAVPRSSPDWAQ----COOLSRNL-----CMLANNAHAPAGHM - 54

DB 9 LLILPTCLSGATESASSPDCAQPKFWCOSLEQRIQCRALGHCLQEWNHGAGNDLCQ 68

QY 55 -----NLLREDEDEETKNNYPRIOCEDGCDPQGLKDNSQFCQLQTROGLAFYKLSD 108

DB 69 ECDIVHLTKTKDEDQFDTRTKFLQECDILPLK----LLVPRQRQVLDVPLV-ID 123

QY 109 IFRGEPAILLPDSMPMEQHTSLIGLSQLOPEDHPRETQMPSSQQWORPLRSKILR 168

DB 124 YQQGQ--IKPKAICs -HVGLCPLGQ-TKPKQPKPEMDAIPN-----PLINKLVLP 169

QY 169 SLQ-AFLA 175

DB 170 ALPGAFAL 177

RESULT 8

IL6_PIG STANDARD; PRT; 212 AA.

RL	Eur. J. Biochem. 176:187-197(1988).	RESULT 11
RN [8]	SEQUENCE OF 66-75; 78-84 AND 128-148.	IL6_RAT
RP MEDLINE=90147691; PubMed=2948184;	ID P26070;	STANDARD;
FX	AC F20607;	PRT; 211 AA.
RA Jahnem W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;	DT 01-FEB-1991 (Rel. 17, Created)	
RT Internal amino acid sequencing of proteins by <i>in situ</i> cyanogen bromide cleavage in polyacrylamide gels.";	DT 01-FEB-1991 (Rel. 17, Last sequence update)	
RT Biochem. Biophys. Res. Commun. 166:139-145(1990).	DT 15-JUN-2002 (Rel. 41, Last annotation update)	
RL RN [9]	DE Interleukin-6 precursor (IL-6).	
RP SEQUENCE OF 25-45.	GN IL6 OR IL-6.	
FX MEDLINE=87092311; PubMed=2789217;	OS Rattus norvegicus (Rat).	
RA van Stieck J., Caaphas S., Vink A., Uttenhove C., Coulie P.G.,	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RA Rubina M.R., Simpson R.J.;	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.	
RT "Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine with growth factor activity for B-cell	NCBI_TaxID=10116;	
RT hybridomas."	RN [1]	
RL proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).	RP SEQUENCE FROM N.A.	
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL	RX MEDLINE=89380206; PubMed=2789217;	
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION	RA Northemann W., Bracioli T.A., Hattori M., Lee F., Fey G.H.;	
OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND	RT Structure of the rat interleukin 6 gene and its expression in	
PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN	RT macrophage-derived cells.;	
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.	CC J. Biol. Chem. 264:16072-16082(1989).	
CC -1- SUBCELLULAR LOCATION: Secreted.	-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL	
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.	FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration	OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND	
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION	
CC use by non-profit institutions as long as its content is in no way	IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.	
CC modified and this statement is not removed. Usage by and for commercial	-1- SUBCELLULAR LOCATION: Secreted.	
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
DR EMBL; X06203; CAA19560_1; -	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
DR EMBL; M20572; AAA39302_1; -	use by non-profit institutions as long as its content is in no way	
DR EMBL; X51457; CAA5824_1; -	modified and this statement is not removed. Usage by and for commercial	
DR EMBL; J03783; AAA19301_1; -	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
DR EMBL; X53545; CAA3841_1; -	CC	
DR EMBL; M24221; AAA68814_1; -	CC	
DR PIR: A30531; TCMS6.	CC	
DR HSSP; P05231; IALU.	CC	
DR MGI; MGI: 96555; -	DR HSSP; P05231; IALU.	
DR InterPro; IPR003573; IL6_MGF_GCSF.	DR InterPro; IPR003573; IL6_MGF_GCSF.	
DR InterPro; IPR003574; Interleukin-6.	DR InterPro; IPR003574; Interleukin-6.	
DR PRNTS; PR00489; IL6.	DR PRNTS; PR00489; IL6.	
DR PRODOM; PD00433; IL6GCSFMGF.	DR PRODOM; PD00433; IL6GCSFMGF.	
DR SMART; SM00126; IL6.	DR SMART; SM00126; IL6.	
DR PROSITE; PS00224; INTERLEUKIN_6.	DR PROSITE; PS00224; INTERLEUKIN_6.	
DR PROSITE; PS00254; INTERLEUKIN_6.	KW Cytokine; Growth factor; Glycoprotein; Signal.	
KW Cytokine; Growth factor; Glycoprotein.	FT SIGNAL	
FT SIGNAL	FT CHAIN	
FT DISULFID	FT DISULFID	
FT DISULFID	FT DISULFID	
SQ SEQUENCE 211 AA: 24384 MW; BBB47DDA9B8678TA CRC64;	SQ SEQUENCE 211 AA: 109 BY SIMILARITY.	
Query Match 9.28; Score 96; DB 1; Length 211;	Query Match 8.88; Score 91; DB 1; Length 211;	
Best Local Similarity 25.5%; Pred. No. 0.04; Gaps 9;	Best Local Similarity 24.5%; Pred. No. 0.12; Gaps 9;	
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;	Matches 39; Conservative 27; Mismatches 63; Indels 30; Gaps 9;	
QY 35 QESRNLCMLAWNAHAPAGHMNLREEEDEETKNN--VPRIOCEDGCDPQGLKDNSQFCLO 92	QY 35 QLSRNLCMLAWNAHAPAGHMNLREEEDEETKNN--VPRIOCEDGCDPQGLKDNSQFCLO 92	
Db 64 EMRKELC---NGNSDC--MN---NDDALAENNLKLPEIQRDGYQTGY-NOEICLL 111	Db 64 EMRKELC---NGNSDC--MN---SDIFKGEPALLPDSPMPEQLHTSLLGLSOLQPEDH--PR 143	
QY 93 RIROGLAFYKHLID----SEIFKGEPALLP-----DSPMEQLHTSLL--GLSQ 134	QY 93 RIROGLAFYKHLID----SEIFKGEPALLP-----DSPMEQLHTSLL--GLSQ 134	
Db 112 KFSSLGEYHSLEYMRKNNKLKARVQDRTETLIHNFQEVKD:HKVLPPTISN 171	Db 112 KFSSLGEYHSLEYMRKNNKLKARVQDRTETLIHNFQEVKD:HKVLPPTISN 171	
QY 135 LLQEDHPRETQOMPSSQWQPLRSKTLRSQOFLAIARR 179	QY 144 ETQQ--MPSLSSQQWQPLRSKTLRSQOFLAIARR 179	
Db 172 ALLTD-----KLESQEWLRKTQFILKSLEEFLKVTLR 206	Db 168 PTSNALLMKLESQEWLRKTQFILKSLEEFLKVTMR 206	
		RESULT 12
		IL6_PHOV

ID	IL6_PHOVT	STANDARD;	PRT;	209 AA.
AC	Q28819;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Interleukin-6 precursor (IL-6) (Fragment).			
GN	IL6.			
OS	Phoca vitulina (Harbor seal); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.			
OC	OC			
NCBI_TaxID	3720;			
OX	OX			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9616301B; PubMed=8575817;			
RA	King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D., Stott J.L., Ferrick D.A.; Molecular cloning and sequencing of interleukin 6 cDNA fragments from the harbor seal (<i>Phoca vitulina</i>), killer whale (<i>Orcinus orca</i>), and Southern sea otter (<i>Enhydra lutris nereis</i>).;			
RT	Immunogenetics 43:190-195 (1996).			
RL	-!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO Ig- SECRETING CELLS, IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).;			
CC	-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.1sb-sib.ch/announce/ or send an email to license@1sb-sib.ch).			
CC	-----			
CC	EMBL: L46802; AAB01430 1; -.			
DR	HSSP; P05231; IL6;			
DR	InterPro: IPR003574; IL6_MGP_GCSF.			
DR	InterPro: IPR003574; Interleukin_6.			
DR	PRINTS: PR00433; IL6; 1.			
DR	PRODOM: PD004356; Interleukin_6; 1.			
DR	SMART: SM00126; IL6; 1.			
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.			
KW	Cytochrome; Glycoprotein; Growth factor; signal.			
FT	NON_TER 1 1 BY SIMILARITY.			
FT	SIGNAL <1 26 BY SIMILARITY.			
FT	CHAIN 27 209 INTERLEUKIN-6.			
FT	DISULFID 69 75 BY SIMILARITY.			
FT	DISULFID 98 108 BY SIMILARITY.			
FT	SEQUENCE 209 AA: 23483 MW: 7514922E43B48E9 CRC64;			
Query Match	8.7% Score 90; DB 1; Length 209;			
Best Local Similarity	27.3% Pred. No. 15; Mismatches 53; Indels 34; Gaps 10; Matches 42; Conservative			
Qy	52 GHMLLREE-----EDEE----TRNNK-----WVPIQEDGCGDQGLKDNSQRQLQRQG 97			
Db	59 GKISALRKEMCDKYNCDSKEAENNLRLKLAERDGCFQSFGF--NOETCLTRITG 116			
Qy	98 LAFYKHL--LDSDFIKGEPALLPDSPMEQLHFLSLLQLSLOPE-----DHPRET 145			
Db	117 LEFOIHLKTYQAN YEGNK --EDANSYFISTRL--LVQMMLKKVKVSQDEVVTPDPFTDT 170			
Qy	146 QOMPSSSQWQPLRSKILRSQAFIAAR 179			
Db	171 SLQAILAKDQKLHHTIHLILRSLEDLFQFSLR 204			
RESULT	13 FRZ3_DROME			
ID	FRZ3_DROME STANDARD;	PRT;	581 AA.	

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartman R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*,"; *Science* 287:2185-2195 (2000);
-!- FUNCTION: receptor for Wnt proteins. Most of frizzled receptors are coupled to the beta catenin canonical signaling pathway, which leads to the activation of disheveled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. Required to coordinate the ciliae of epidermal cells to produce a parallel array of cuticular hairs and bristles.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Wing, leg and eye imaginal disks. In embryos, expressed is seen in brain, proventricular, Malpighian tubules, anal plate and visceral mesoderm of parasegment 8.
CC -!- DEVELOPMENTAL STAGE: Expressed in embryos from stage 11 and in larvae.
CC -!- DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
CC -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to License@isb-sib.ch).

EMBL: AB018565; BAA8677_1;
DR EMBL: AF195242; AAF62250_1; -;
DR EMBL: AF031583; CAA20896_1; -;
DR EMBL: AE003418; AAF45547_1; -;
DR EMBL: AE003418; AAG22363_1; -;
DR FlyBase: FBgn0021343; fz3;
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF01334; Frizzled; 2.
DR PRINTS: PR00489; FRIZZLED.
DR SMART: SM00063; FRI; 1.
DR PROSITE: PS50038; FZ_1.
DR PROSITE: PS50061; G-PROTEIN_RECEP_F2_4; 1.
KW Multigene family; Receptor; G-protein coupled receptor; Transmembrane Developmental protein; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 19 FRIZZLED PROTEIN 3.
FT CHAIN 20 581 FRIZZLED PROTEIN 3.
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 1 (POTENTIAL).
FT DOMAIN 259 270 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 271 291 2 (POTENTIAL).
FT DOMAIN 292 321 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 322 342 3 (POTENTIAL).
FT DOMAIN 343 359 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 360 380 4 (POTENTIAL).
FT DOMAIN 381 393 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 394 414 5 (POTENTIAL).
FT DOMAIN 415 442 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 443 463 6 (POTENTIAL).
FT DOMAIN 464 488 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 489 509 7 (POTENTIAL).
FT DOMAIN 510 581 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 335 156 F2.
FT DOMAIN 403 410 POLY-LEU.
FT SITE 579 581 PDZ-BINDING.
FT CARBOHYD 54 54 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC . . .) (POTENTIAL).
FT VARSPPLIC 1 55 MISSING (IN SHORT ISOFORM).
FT VARSPPLIC 56 73 TALPNAIAGHQNLEELQ -> MDRKTKERCVGIDYLIP (IN SHORT ISOFORM).
FT CONFLICT 56 56 T -> I (IN REF 1).
FT CONFLICT 192 192 A -> V (IN REF 1).
FT CONFLICT 276 276 L -> P (IN REF 1).
FT CONFLICT 304 304 G -> W (IN REF 4).
FT CONFLICT 376 376 A -> V (IN REF 1).
SQ SEQUENCE 581 AA; 63251 MW; 0748BBF2A9E3F93 CRC64;

Query Match 8 6%; Score 89.5; DB 1; Length 581;
Best Local Similarity 29.0%; Pred. No. 0.59; Gaps 10;
Matches 45; Conservative 23; Mismatches 60; Indexes 27; Gaps 10;

QY 6 AVIMWLLPVWTQGLA-----VPRSSSPDMAQCOOLSRNLCM-LAWNHA---PAG 52
Db 4 ASILILHITWAVATIAANGAGHNGPVASSAGPNQLQQIAVACQGUGYNTALPNIAG 63

QY 53 HMNLRLREEDDEETKNNVPRIOCEDGCDPQG--LKDNQSOF--CLQRTRQGLAFYKHLDSD 108
Db 64 HTNQL-EAEQIQLKLPLI-ESGCSRARFLCSSLPLCPDPVRPAACKLCLCT- 118

QY 109 IFKCEPALIPDSPE--QIHTSLIGLSQLQPEDH 141
Db 119 -VRGE--CMENAPPLEMWPSFLNCGDPQPEKH 150

RESULT 14
ID NH20_CAEEL STANDARD; PRT; 457 AA.
AC Q09765; Q9GT16;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nuclear hormone receptor family member nrh-20.
GN NHR-20 OR F4301_4.
OS Caenorhabditis elegans.
OC Rhabditidae; Plecterinae; Caenorhabditis.
OC NCBItaxID=6239;
RN [1] REVISIONS.
RN Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN [2] SEQUENCE FROM N.A.
RN [3] STRAIN=Bristol N2;
RN RA Jassal B.; Smith A.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN [1] SEQUENCE OF 4-457 FROM N.A.
RA Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;
RT "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical compatibility with the ligand-binding domain fold";
RT Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: ORPHAN NUCLEAR RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use.

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; Z66937; CAA87058.2; .
 DR HSSP; P20393; 1A6Y.
 DR WompPeP; P425C1_4'; CE28025.
 DR InterPro; IPR00536; Hormone_rec_lig.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR PFAM; PF00104; hormone_rec; 2.
 DR Pfam; PF00105; zf-c4; 2.
 DR PRINTS; PRO0047; STR01FINGER.
 DR PRODOM; PD00033; Znf_C4steroid; 1.
 DR SMART; SM00430; HOLL; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSTE; PS00031; NUCLEAR_RECECTOR; FALSE_NEG.
 Receptor; transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger.

FT DNA_BIND 19 85 NUCLEAR_RECECTOR-TYPE.
 FT ZN_FING 19 40 C4-TYPE.
 FT ZN_FING 56 80 C4-TYPE.
 SQ SEQUENCE 457 AA; 52029 MW; C9E3C012764BBBF1 CRC64;

Query Match Score 89; DB 1; Length 457;
 Best Local Similarity 25.9%; Pred. No. 0.49; Length 457;
 Matches 37; Conservative 17; Mismatches 39; Indels 50; Gaps 7;
 QY 32 QCOQLSRNLCLMIAWNNAHAPAGHMNLREEDDEETKNNVPRQCDGCDPQGLKDNSQFCI 91
 Db 88 ECVQKRSR-----NRKIPKHMNLREDQIKMEYD-----ECKFECGSDQDDNSPLSI 136
 QY 92 QTRQGLAFYKILDSDFKSEPALLP-DSMEQQLHTSLLGLSQQLQEPHHPRETQQMPS 150
 Db 137 EK-----KSPPGILLPNDSM-----MADEKFEDPSDIPS 164
 QY 151 LS-SSQWQR---PLLRSKIL 167
 Db 165 TSGGSTQRLERSPSPKLAESTKL 187

RESULT 15
 CSF3_FEELCA
 ID CSF3_FEELCA STANDARD; PRT; 194 AA.
 AC 002708;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
 GN CSF3.
 OS *Felis silvestris catus* (Cat); Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Pissipedia; Felidae; Felis.
 OX NCBI-TAXID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

RC European shorthair; TISSUE=Lung;
 RA Dunham S.P.; Onions D.E.;
 RT "Cloning, sequencing and expression of feline granulocyte colony
 stimulating factor."
 RL Submitted (Sep-1996) to the EMBL/GenBank/DDBJ databases.
 -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOIETIC CELLS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
 CC CSF INDUCES GRANULOCYTES (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-Glycosylation (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -->
 CC EMBL; Y08558; CAA69853.1; .
 DR HSSP; P35834; 1BGB.
 DR InterPro; IPR003629; GCSE_MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR PFAM; PF00489; IL6.
 DR PRINTS; PRO00433; IL6_GCSF_MGF.
 DR PRODOM; PD0008388; GCSE_MGF; 1.
 DR SMART; SM00126; IL6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.
 FT NON_TER 1 1 POTENTIAL.
 FT SIGNAL <1 20 GRANULOCYTE COLONY-STIMULATING FACTOR,
 FT DISULFID 21 194 BY SIMILARITY.
 FT DISULFID 56 62 BY SIMILARITY.
 FT CARBOHYD 84 94 O-LINKED (GALAC, .). (BY SIMILARITY).
 SQ SEQUENCE 194 AA; F72B/AB3DAE7385E C864;
 Query Match Score 8.3%; Score 86.5; DB 1; Length 194;
 Best Local Similarity 28.3%; Pred. No. 0.29;
 Matches 34; Conservative 20; Mismatches 51; Indels 15; Gaps 5;
 QY 78 CDPOGLKINSOFLQFLQRGLAFYKHLIDSDFIKGEPAELLDPSPMBOLHTSLGLSQLQ 137
 Db 84 CSSQALQLTG--CLROLHSGLFLYQGLQA-LAGISPELAPLTDMLQLDITDFAINTWQO 140
 QY 138 PED----HPRTEQMMSSQWOPPLRSKILSLOQAFIAIAARVEHGAATLTP 191
 Db 141 MEDVGMAPAVPPQTGTMPTFTSA-FQRAGGTIVASNLQSLEVAYRALRH---FTKP 194
 Search completed: November 20, 2002, 11:53:25
 Job time : 9.14545 secs

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:20 ; Search time 26.9818 Seconds
(without alignments)
1496.757 Million cell updates/sec

Title: US-09-658-699-4
Perfect score: 1038
Sequence: 1 MLDCAVTIMLMLPWTQGL.....AARYFAAGAAATLTPLVPTA 196

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rabbit;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: sp_unclassified;*
- 15: sp_rvirus;*
- 16: sp_bacteriP;*
- 17: sp_archeap;*

Result No.	Score	Query	Match	Length	DB ID	Description	RT
1	1038	100.0	196	11	Q9FBQ14	Q9eqI4 mus musculus	RP
2	915	88.2	196	11	Q9IZ84	Q91z84 rattus norvegicus	RN
3	718.5	69.2	189	4	Q9RA5	Q9h2a5 homo sapiens	SEQUENCE FROM N.A.
4	717.5	69.1	189	4	Q9NF7	Q9npf7 homo sapiens	RP
5	663.5	63.9	193	6	Q9NZH9	Q9n2h9 sus scrofa	RA
6	113.5	10.9	208	6	Q9XT80	Q9xt80 delphinapterus	RL
7	106	10.2	207	6	Q9MYZ7	Q9myz7 canis familiaris	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
8	98	9.4	212	11	Q9IZL3	Q91z13 sigmodon hirsutus	DR
9	95	9.2	210	11	Q9WQ8	Q9wgq8 mesocricetus auratus	MGI:1932410; IL123a; AAH19951.1; -
10	91	8.8	209	6	Q9TH3	Q9th3 aotus lemur	DR
11	90	8.7	241	6	Q9MZR1	Q9mr1 oryctolagus cuniculus	InterPro:IPR003573; IL16_MGF_GCSF.
12	89.5	8.6	1217	10	Q94I37	Q94i37 oryza sativa	SMART:SM00126; IL6; 1.0
13	89	8.6	4306	11	Q9JJ79	Q9ij79 rattus norvegicus	SEQUENCE 196 AA; 2201 MW;
14	86.5	8.3	195	6	Q9GJU0	Q9gju0 felis silvestris	DAE4A318A2DD3B7C CRC64;
15	86.5	8.3	353	10	Q9SX30	Q9sx30 arabidopsis	Query Match 100.0%; Score 1038; DB 11; Length 196;
16	86.5	8.3	354	10	Q8V2S3	Q8vzs3 arabidopsis	Best Local Similarity 100.0%; Prcd. No. 2e-101; Mismatches 0; Indels 0; Gaps 0;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	RT
1	1038	100.0	196	11	Q9FBQ14	Q9eqI4 mus musculus	Biological Activities Similar as Well as Distinct from IL-12."
2	915	88.2	196	11	Q9IZ84	Q91z84 rattus norvegicus	NCBI_TaxID=10090;
3	718.5	69.2	189	4	Q9RA5	Q9h2a5 homo sapiens	[1]
4	717.5	69.1	189	4	Q9NF7	Q9npf7 homo sapiens	SEQUENCE FROM N.A.
5	663.5	63.9	193	6	Q9NZH9	Q9n2h9 sus scrofa	RA
6	113.5	10.9	208	6	Q9XT80	Q9xt80 delphinapterus	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
7	106	10.2	207	6	Q9MYZ7	Q9myz7 canis familiaris	DR
8	98	9.4	212	11	Q9IZL3	Q91z13 sigmodon hirsutus	EMBL; BC019953; AAH19951.1; -
9	95	9.2	210	11	Q9WQ8	Q9wgq8 mesocricetus auratus	MGI:1932410; IL123a; AAH19951.1; -
10	91	8.8	209	6	Q9TH3	Q9th3 aotus lemur	InterPro:IPR003573; IL16_MGF_GCSF.
11	90	8.7	241	6	Q9MZR1	Q9mr1 oryctolagus cuniculus	SMART:SM00126; IL6; 1.0
12	89.5	8.6	1217	10	Q94I37	Q94i37 oryza sativa	SEQUENCE 196 AA; 2201 MW;
13	89	8.6	4306	11	Q9JJ79	Q9ij79 rattus norvegicus	DAE4A318A2DD3B7C CRC64;
14	86.5	8.3	195	6	Q9GJU0	Q9gju0 felis silvestris	Query Match 100.0%; Score 1038; DB 11; Length 196;
15	86.5	8.3	353	10	Q9SX30	Q9sx30 arabidopsis	Best Local Similarity 100.0%; Prcd. No. 2e-101; Mismatches 0; Indels 0; Gaps 0;
16	86.5	8.3	354	10	Q8V2S3	Q8vzs3 arabidopsis	

QY	1	MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60 : : : : : : : : : : : 1 MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60	RX MEDLINE=2015-67322; PubMed=1114383; RA OPPMANN B., LESIUS R., BIOM B., THIANS J.C., XU Y., HUNTE B., VEGA F., RA YU N., WANG J., SINGH K., ZONIN F., VAISBERG E., CHURAKOVA T., RA LIU M.-R., GORNICK D., WAGNER J., ZURAWSKI S., LIU Y.-J., ABRAMS J.S., RA MOORE K.W., RENNICK D., DE WAAL-MALEFYT R., HANNUM C., RA KASTELEIN R.A.; RT "Novel p19 protein Engages IL-12p40 to Form a Cytokine IL-23," with RT Biological Activities Similar as Well as Distinct from IL-12.";
QY	61	EDEEFKNNVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120 61 EDEEFKNNVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120	RT Novel p19 protein Engages IL-12p40 to Form a Cytokine IL-23," with RT Biological Activities Similar as Well as Distinct from IL-12.";
QY	121	PMEQLTSLGLSOLLQPEDHPRETOQMPSLSSQQWORPLRSKILRSQAFALAAERV 180 121 PMEQLTSLGLSOLLQPEDHPRETOQMPSLSSQQWORPLRSKILRSQAFALAAERV 180	DR InterPro; IPR03573; IL6_MGF_GCSF.
QY	181	FAHGAATLTEPLVPTA 196 181 FAHGAATLTEPLVPTA 196	DR SMART; SM00126; IL6_1; SQ SEQUENCE 189 AA; 20744 MW; BFB56CF042D4C1EA CRC64;
Db	Db	Query Match 69.2%; Score 718.5; DB 4; Best Local Similarity 74.6%; Pred. No. 9.3e-68; Matches 141; Conservative 14; Mismatches 33; Indels 1; caps 1;	Query Match 69.2%; Score 718.5; DB 4; Best Local Similarity 74.6%; Pred. No. 9.3e-68; Matches 141; Conservative 14; Mismatches 33; Indels 1; caps 1;
QY	Q91284	PRELIMINARY; PRT; 196 AA. AC Q91284; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE InterLinkin 23.	QY 1 MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60 : : : : : : : : : DB 1 MLGSRAVMLLLPLWTAQGRAVPGGSSPAWTCQQLSOKLCTLAWSAHPLVGHMD-LREE 59
OS	Rattus norvegicus (Rat)	QY 61 EDEETKNNVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120 61 EDEETKNNVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120	DB 60 GDEBETNDVPHIQGCGDPOGLRDNQFCQRIQGLFLITEKLGSDFITGEPSLIPDS 119
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus .	QY 121 PMEQLHTSLGLSOLLQPEDHPRETOQMPSLSSQQWORPLRSKILRSQAFALAAERV 180 1: : : : : : : : : DB 120 PVAQLHASLGLSOLLQPEGHHWETOQIPSLSPQWPWORLDRLRFKILRSQAFVAAERV 179	QY 181 FAHGAATLT 189 : : DB 180 FAHGAATLS 188
NCBI_TaxID=10116;	[1]	RESULT 2 SEQUENCE FROM N.A. STRAIN=LEN; TRAN G., Hodgkinson S. ; RT "Rattus norvegicus IL-23 mRNA." ; RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases. DR EMBL; AY05379; ALI18225.1; . SEQUENCE 196 AA; 21986 MW; 188FF74BC409A961 CRC64;	RESULT 4 Q9NPF7 PRELIMINARY; ID Q9NPF7 AC Q9NPF7; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update) DE SGRF precursor. . GN SGRF. OS Homo sapiens (Human). RA Hirata Y., Kosuge Y.; OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo . OX NCBI_TaxID=9606; RN [1] RP SEQUENCE FROM N.A. RC TISSUE=SPLEEN; RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases. DR EMBL; AB030000; BRA93686.1; . DR AB030001; BRA93687.1; . DR InterPro; IPR03573; IL6_MGF_GCSF . DR SMART; SM00126; IL6_1. KW Signal. FT SIGNAL 1 19 POTENTIAL. FT CHAIN 20 189 SGRF. SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188BC1B9F CRC64;
QY	1	MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60 : : : : : : : : : 1 MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60	Query Match 69.1%; Score 717.5; DB 4; Best Local Similarity 74.6%; Pred. No. 1.2e-67; Matches 141; Conservative 14; Mismatches 33; Indels 1; caps 1;
Db	Db	QY 61 EDEETKNSDVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120 61 EDEETKNSDVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120	QY 1 MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60 : : : : : : DB 1 MLGSRAVMLLLPLWTAQGRAVPGGSSPAWTCQQLSOKLCTLAWSAHPLVGHMD-LREE 60
QY	121	PMEQLTSLGLSOLLQPEDHPRETOQMPSLSSQQWORPLRSKILRSQAFALAAERV 180 121 PMEQLTSLGLSOLLQPEDHPRETOQMPSLSSQQWORPLRSKILRSQAFALAAERV 180	QY 181 FAHGAATLTEPLVPTA 196 181 FAHGAATLTEPLVPTA 196
Db	Db	DR InterPro; IPR03573; IL6_MGF_GCSF . DR SMART; SM00126; IL6_1.	DR InterPro; IPR03573; IL6_MGF_GCSF . DR SMART; SM00126; IL6_1.
RESULT 3 Q9H2A5	PRELIMINARY;	PRT; 189 AA.	KW Signal. FT SIGNAL 1 19 POTENTIAL. FT CHAIN 20 189 SGRF. SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188BC1B9F CRC64;
ID	Q9H2A5;	AC Q9H2A5;	Query Match 69.1%; Score 717.5; DB 4; Best Local Similarity 74.6%; Pred. No. 1.2e-67; Matches 141; Conservative 14; Mismatches 33; Indels 1; caps 1;
AC	Q9H2A5;	DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE InterLinkin 23 p19 subunit.	QY 1 MLDCRAVIMWLPLWTOGLAVERPSSSPDWAOQQLSRNLCMALAWNAHAPAGHMLLREE 60 : : : : DB 1 MLGSRAVMLLLPLWTAQGRAVPGGSSPAWTCQQLSOKLCTLAWSAHPLVGHMD-LREE 59
OS	Homo sapiens (Human)	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo . OX NCBI_TaxID=9606;	QY 61 EDEETKNNVPRIQEDGCDPOGLKDNSQFCLOTRQGLAFYKHLDSDFIKGEPALLPDS 120 : : : : RN [1] RP SEQUENCE FROM N.A.

Db	60	GDEETTNDYPHIQCGDGPGLRDNQSFCLRQIHQGLIFYKLGSDFITGEPSLLPDS	119	RL Submitted (JUL-1998) to the EMBL/GenBank/DBBJ databases.
Qy	121	PMEQLHTSLLGSLQQLQPDDPRETQMPSSQWORPLRSKILRSLOAFLAARY	180	DR AF07643; AAD42929.1; -.
Db	120	PVGQHASLLGSLQQLQPEGHMETQQIPSLFSQPMQRLLRFKILRSLOAFVAALARV	179	DR HSSP; P05231; IL6.
Qy	181	FAHGAATLT 189		DR InterPro; IPR003573; IL6.
Db	180	FAHGAATLS 188		DR pfam; PF00489; IL6; 1.
RESULT 5				
Q9NZH9		PRELIMINARY;	PRT;	193 AA.
ID				
AC	Q9NZH9;			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DE	SGRF.			
GN				
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hiraga Y.; Kosuge Y.;			
RT	"SGRF: a novel member of the IL-6/G-CSF family.";			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBBJ databases.			
DR	AB030022; BAQ93688.1; -.			
InterPro	IPR003573; IL6_MGF_GCSF.			
SMART	SM00126; IL6; 1.			
SEQUENCE	193 AA;	21132 MW;	05F28DE94810B9E1 CRC64;	
Qy	1	MEDCRV--IMMLWLPWTOGLAVPRSSSPWAOCQLSRNLCMIAWNAAHPAGHMNL 57		OS Canis familiaris (Dog).
Db	1	M1LSRAYWMLLLEWTWSQRAVEPGSSPAWAQQLSQCQLTAWTAHPMGHVDLP 60		OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Qy	58	RREFEEDETKNNVPRIOCEDGCDPOGLKDNSOFLCLRQIYKHLSDIFKEPEALL 117		OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Db	61	REEGDDETTSEVPHIQCGDGPQGLRDNSOSCQLOIHQLYFVERKLGSDFITGEPSLH 120		NCB_TaxID=9615;
Qy	118	PDSPEQIHTSLLGSLQQLQPDDPRETQMPSSQWORPLRSKILRSLOAFLA 177		RN SEQUENCE FROM N.A.
Db	121	PDSVYQGHASLLGSLQQLQPEGHMETQQIPSLFSQPMQRLLRFKILRSLOAFVAAVA 180		RA Youn H.-Y., Shin I.-S.;
Qy	178	ARYFAHGAATLT 190		RT Canine IL-6 mRNA.;
Db	181	ARYFAHGAATLSQ 193		RL Submitted (JUN-2000) to the EMBL/GenBank/DBBJ databases.
RESULT 6				
Q9XTB0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XTB0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA	St-Laurent G.; De Guise S.; Fournier M.; Archambault D.;			
RU	"Molecular cloning and phylogenetic analysis of beluga whale (Delphinapterus leucas) interleukin 6.";			
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			
OC	Monodontidae; Delphinapterus.			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RA				
RU				
RT				
Q9XBT0		PRELIMINARY;	PRT;	208 AA.
ID				
AC	Q9XBT0			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DE	Interleukin 6.			
OS	Delphinapterus leucas (Beluga whale).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;			

Query Match	8.6%	Score 89;	DB 11;	Length 4306;			
Best Local Similarity	28.0%	Pred. No. 10;					
Matches	40;	Conservative	20;	Mismatches	5;	Indels	28;
						Gaps	8;
Qy	53	HANLLRBEEDESTKNNVPRICEDGCDPOGIKDNQFCL--QRIRQGLAFYKHLLDSD--	108				
Db	20	YFGLRPELWDQTPLNSCPEVN-----NFLDDGQMLLRLVRQSADLAFL-SNTIDFDDT	71				
Qy	109	-TFKGEPALLPPSPMQLLGLQSLGQHDTRETOOM---PSLSSSQQWQR	159				
Db	72	KDKVLVPEFKLRPEVITDG--NLHNHLVSSMLESPINSLYQAVRQVFAPMLIKDQEWSR	128				
Qy	160	---PLRSKILRLSQQAFLAAR	179				
Db	129	NFDPKLQN-LLSELEAGLVVLR	150				
RESULT 14							
Q9GSU0	ID	Q9GJU0	PRELIMINARY;	PRT;	195 AA.		
AC	Q9GJU0;						
DT	01-MAR-2001	(TREMBLrel. 16,	Created)				
DT	01-MAR-2001	(TREMBLrel. 16,	Last sequence update)				
DT	01-DEC-2001	(TREMBLrel. 19,	Last annotation update)				
DE	Granulocyte colony-stimulating factor precursor.						
GN	G-CSF.						
OS	Felis silvestris catus (Cat).						
EC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.						
OX	NCB_--TaxID=9685;						
SEQUENCE FROM N.A.							
Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K.,							
RA	Tsujimoto H., Hasegawa A., Ueda S.;						
RT	"Molecular cloning and expression of the cDNA encoding feline						
RT	granulocyte colony-stimulating factor.";						
RT	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RA	Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K.,						
RA	Tsujimoto H., Hasegawa A., Ueda S.;						
RT	"Molecular cloning and expression of the cDNA encoding feline						
RT	granulocyte colony-stimulating factor.";						
RT	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.						
RN	[2]						
RA	SEQUENCE FROM N.A.						
RA	Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K.,						
RA	Tsujimoto H., Hasegawa A., Ueda S.;						
RT	"Molecular cloning and expression of the cDNA encoding feline						
RT	granulocyte colony-stimulating factor.";						
RT	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.						
RL	[2]						
DR	PRINTS; PRO0433; IL6CSFMGF.						
DR	Prodom; PD003388; GCSF_MGF.1.						
DR	SMART; SM00126; IL6.1.						
DR	PROSTINE; IPRO03629; GCSF_MGF.						
DR	InterPro; IPRO03573; IL6_MGF_GCSF.						
DR	InterPro; IPRO0489; IL6.1.						
FT	SIGNAL 1 21 POTENTIAL.						
SQ	SEQUENCE 195 AA; 21255 MW; 544C662909412FCF CRC64;						
Query Match	8.3%	Score 86.5;	DB 6;	Length 195;			
Best Local Similarity	28.3%	Pred. No. 0.4;					
Matches	34;	Conservative	20;	Mismatches	51;	Indels	15;
						Gaps	5;
Qy	78	CDPQKLKDNSQFLCLRIGRQLAFYKHLLDIFKGERALPDSPMEQLHTSLSLGSQLL	137				
Db	85	CSSQDALQLTG--CLRQLHSGLFLYQGLLQA-LAGISPLAFTLDMQLDITDFAINTWQ	141				
Qy	138	PED-----HPRETQMPSSQSSQWQRPLRSKILSRLQAFIAARVFAAHAAITEP	191				
Db	142	MEDVGMAPAWPPGTMTPTSA -FORRAGGLIVASNLQSLEVRAIRH ---FTKP	195				

SUMMARIES									
Result No.	Score	Query	Match	Length	DB	ID	Description	\$	
1	1038	GenCore version 5.1.3	100.0	196	20	AAV29784	Mouse interleukin-	XX	XX
2	1038	Copyright (C) 1993 - 2002 Compugen Ltd.	100.0	196	20	AAW5003	Mouse interleukin-	XX	XX
3	1038	OM protein - protein search, using sw model	100.0	196	21	AAH01982	Murine interleukin	PD	12-AUG-1999
4	1038	Run on: November 20, 2002, 11:48:39 ; Search time 33.6 Seconds (without alignments) 777.295 Million cell updates/sec	100.0	196	22	AAT47121	Human interleukin	XX	05-FEB-1999
5	718.5	Perfect score: 1038	MLDRCAVIMLRLPPWVTQGL.....ARVFAHGAATLTLEPLVYPTA	196	17	AAV29783	Human interleukin	XX	13-MAY-1998
6	718.5	Sequence: 1 MLDRCAVIMLRLPPWVTQGL.....ARVFAHGAATLTLEPLVYPTA	196	17	AAV29784	Mouse interleukin	XX	PR	06-FEB-1998
7	718.5	Scoring table: BLASTM62	Gapop 10.0 , Gapext 0.5	196	17	AAW5013	Pig interleukin	XX	98US-007194
8	718.5	Searched: 908470 seqs, 133250620 residues	908470	196	17	AAW9304	Mature porcine int	XX	98US-0073941
9	717.5	Total number of hits satisfying chosen parameters:	908470	196	17	AAW01983	Sequence of ovine	XX	-
10	717.5	Minimum DB seq length: 0	908470	196	17	AAR22125	Sheep interleukin	XX	-
11	717.5	Maximum DB seq length: 2000000000	908470	196	17	AAW95002	Bovine interleukin	XX	-
12	717.5	Post-processing: Minimum Match 0%	908470	196	17	AAW9512	Mouse interleukin	XX	-
13	717.5	Maximum Match 100%	908470	196	17	AAW9342	Cytokine mIL-6	XX	-
14	717.5	Listing first 45 summaries	908470	196	17	AAW9347	Murine interleukin	XX	-
15	717.5	Database : A_Geneseq_101002:*	908470	196	17	AAR33385	Human interleukin	XX	-
16	717.5	1: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1980.DAT:*	908470	196	17	AAR33386	Human interleukin	XX	-
17	717.5	2: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1981.DAT:*	908470	196	17	AAR49040	Human interleukin	XX	-
18	717.5	3: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1982.DAT:*	908470	196	17	AAR31997	Human interleukin	XX	-
19	717.5	4: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1983.DAT:*	908470	196	17	AAR72212	Human interleukin	XX	-
20	717.5	5: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1984.DAT:*	908470	196	17	AAW016191	Human interleukin	XX	-
21	717.5	6: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1985.DAT:*	908470	196	17	AAU16606	Human interleukin	XX	-
22	717.5	7: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1986.DAT:*	908470	196	17	AAW00131	Feline G-CSF sequ	XX	-
23	717.5	8: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1987.DAT:*	908470	196	17	AAW5006	A granulocyte colo	XX	-
1	717.5	9: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1988.DAT:*	908470	196	17	AAR02471	Novel human diagno	XX	-
10	717.5	10: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1989.DAT:*	908470	196	17	ABG15221	Chimeric interleuk	XX	-
11	717.5	11: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1990.DAT:*	908470	196	17	ABR80147	IL-3 containing fu	XX	-
12	717.5	12: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1991.DAT:*	908470	196	17	AAW77391	Human interleukin	XX	-
13	717.5	13: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1992.DAT:*	908470	196	17	AAW00142	Human interleukin	XX	-
14	717.5	14: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1993.DAT:*	908470	196	17	AAV53205	Myelopietin (MPO)	XX	-
15	717.5	15: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1994.DAT:*	908470	196	17	AAE13999	Chimeric receptor	XX	-
16	717.5	16: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1995.DAT:*	908470	196	17	AAW78103	Human interleukin	XX	-
17	717.5	17: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1996.DAT:*	908470	196	17	AAW040131	Feline G-CSF sequ	XX	-
18	717.5	18: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1997.DAT:*	908470	196	17	AAW5006	A granulocyte colo	XX	-
19	717.5	19: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1998.DAT:*	908470	196	17	AAY29784	Novel human diagno	XX	-
20	717.5	20: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA1999.DAT:*	908470	196	17	ABG15221	Chimeric interleuk	XX	-
21	717.5	21: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2000.DAT:*	908470	196	17	ABR80147	IL-3 containing fu	XX	-
22	717.5	22: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2001.DAT:*	908470	196	17	AAW77391	Human interleukin	XX	-
23	717.5	23: /SIDS2/gcadata/geneseq/geneseqp-emb1/AA2002.DAT:*	908470	196	17	AAW00142	Human interleukin	XX	-
1	717.5	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	717.5	196	20	AAU12287	Human interleukin	XX	-
2	717.5	2	1038	100.0	196	20	AAV29784	Human interleukin	XX
3	717.5	3	1038	100.0	196	20	AAW5003	Partial Pig interl	XX
4	717.5	4	1038	100.0	196	21	AAH01982	Pig interleukin B3	PD
5	717.5	5	718.5	69.2	189	20	AAT47121	Mature porcine int	XX
6	717.5	6	718.5	69.2	189	21	AAW95002	Sequence of ovine	XX
7	717.5	7	718.5	69.2	189	21	AAB01981	Sheep interleukin	XX
8	717.5	8	718.5	69.2	189	22	AAB74120	Human IL-B30. Hom	XX
9	717.5	9	717.5	69.1	189	21	AAV94966	Human secreted pro	XX
10	717.5	10	717.5	69.1	189	21	AAV54606	SGRF protein seque	PA

ALIGNMENTS

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		
XX		
OS	Mus sp.	
XX		
KEY	Location/Qualifiers	
FT	1..21	
FT	/label= signal	
FT	22..196	
FT	/label= IL-B30	

RESULT 1	AAV29784	Standard; Protein; 196 AA.
ID	AAV29784	
XX		
AC	AAV29784;	
XX		
DT	04-NOV-1999	(first entry)
XX		
DE	Mouse interleukin B30.	
XX		
DNAx soluble receptor subunit 1; DNAX cytokine receptor subunit 1; interleukin B30; DSR51; IL-B30; cytokine receptor; diagnosis; inflammatory disorder; inflammatory response; innate immunity; morphogenetic development; immunological disorder.		

XXX	Kastelein RA,	Mattson JD,	McClanahan TK;	
PPI	WPI;	1999-5-27 306/44.		
XX	DDR	N-PSDB;	AAZ08866.	
XX	XX	New receptor subunits useful in the treatment inflammatory disorders		
XX	XX	Claim 2; Page 27-28; 133pp; English.		
PPS	XX	The present invention describes a composition (I) comprising DNAX cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor subunit I (DCRS1) protein, which together encode a new mammalian cytokine-related receptor (R), or DCRS1 and Interleukin B30 (IL-B30) proteins, or DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1 is useful for screening for ligands (i.e. agonists/antagonists) from a library of compounds, which are useful for modulating the physiology or development of a cell or tissue culture e.g. 9. inflammatory responses, innate immunity and/or morphogenic development. (R) antibodies and ligands are useful for treatment of conditions, especially immunological disorders, associated with conditions exhibiting abnormal expression of (R). (R) is useful as a phosphatase labeling enzyme to label substrates, and the subunits DRS1 and DCRS1 are useful as immunogens for generating antibodies, or as antigens for binding antibodies. Nucleic acids encoding (R) are useful for identifying related DNAs and mRNAs, and variants from other individuals or species. The present sequence represents the specifically claimed mouse IL-B30, for use in the composition of the present invention.		
CC	XX	Sequence 196 AA;		
CC	XX	SQ	Query Match 100.0%; Score 1038; DB 20; Length 196; Best Local Similarity 100.0%; Pred. No. 1.2e 99; Matches 196; Conservative 0; Mismatches 0; Indels 0; Caps 0;	
CC	XX	Db	1 MLDGRAVIMLWLLPWVTOQGLAVPRSSSPDIAQCQLSRNLCMLAWNAHADAGHMNLRE 60 1 MLDGRAVIMLWLLPWVTOQGLAVPRSSSPDIAQCQLSRNLCMLAWNAHADAGHMNLRE 60	
CC	XX	Qy	61 EDEETKNNVPRIQEDGCDDEQGLKDNSQFLQCLRFRQGLARYKHLDSDTFKGEPLLPDS 120 61 EDEETKNNVPRIQEDGCDDEQGLKDNSQFLQCLRFRQGLARYKHLDSDTFKGEPLLPDS 120	
CC	XX	Db	121 PMEQLTLSLIGLSQOLQEPDHPRETQMPSSLSSQWQRLRSKILRSI-QAFLATAARY 180 121 PMEQLTLSLIGLSQOLQEPDHPRETQMPSSLSSQWQRLRSKILRSI-QAFLATAARY 180	
CC	XX	Qy	181 FAHGAATLTFPLYTA 196 181 FAHGAATLTFPLYTA 196	
CC	XX	Db	RESULT 2 AAW5003 AAW5003 standard; Protein; 196 AA. ID ID XX AAW5003 standard; Protein; 196 AA. XX AC AAW5003; XX DT 21-MAY-1999 (first entry) XX DE Mouse interleukin-B30 (IL-B30) polypeptide. XX KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation; inflammatory condition; drug screening; mouse. XX OS Mus sp. XX Key Location/Qualifiers Peptide FT 1..21 FT /note= "signal peptide" Protein FT 22..196 FT /note= "mature protein" XX	

KW inflammatory disease; autoimmune disease; antigen; antibody.
 XX
 OS Mus sp.
 XX Location/Qualifiers
 FH 1..21
 FT Peptide /note= "Signal peptide"
 FT protein /note= "Mature murine IL-B30"
 FT XX
 PN US6060284-A.
 XX PD 09-MAY-2000.
 XX PF 24-JUL-1998; 98US-0122443.
 XX PR 25-JUL-1997; 97US-0053765.
 XX PA (SCH) SCHERRING CORP.
 XX PI Bazan JF;
 XX DR WPI: 2000-364420/31.
 DR N-PSDB; AAA52578.
 XX PT Novel recombinant DNA encoding cytokines especially interleukin-B30
 PT as probes or primers for diagnosing immune disorders including
 PT autoimmune or chronic inflammatory conditions -
 XX PS Claim 1; Column 7-10; 32pp; English.
 CC This sequence represents murine interleukin-B30 (IL-B30). IL-B30
 CC is a novel cytokine, exhibiting significant homology to IL-6 and
 CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical
 CC role in signalling between immune or other cells during an immune
 CC response. The precise role if IL-B30 is not yet known - it is likely to
 CC have either a stimulatory or an inhibitory effect on haematopoietic cells
 CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.
 CC Alternatively, it may affect vascular physiology or development, or have
 CC neuronal effects. IL-B30 its fragments, nucleotides, agonists and
 CC antagonists are useful in the diagnosis and treatment of disorders
 CC associated with abnormal expression or activity of IL-B30 e.g.,
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are
 CC useful for recombinant expression of IL-B30 in a host cell, and as a
 CC source of probes and primers. The IL-B30 probes and primers can be used
 CC to detect levels of IL-B30 expression in samples from patients suspected
 CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may
 CC also be used to identify homologous genes in other species. IL-B30
 CC protein or its fragments are useful as antigens for raising antibodies to
 CC various linear and conformational epitopes. Such antibodies may be used
 CC to detect levels of IL-B30 protein in a sample.
 XX Sequence 196 AA;
 SQ Query Match 100.0%; Score 1038; DB 21; Length 196;
 Best Local Similarity 100.0%; Ptd. No. 1..2e-9;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLDCRAVIMWLPWVTLGLAVPRSSSDWAQQQLSRNLCMLAWNAHAPGHMNLLRE 60
 Db 1 MLDCRAVIMWLPWVTLGLAVPRSSSDWAQQQLSRNLCMLAWNAHAPGHMNLLRE 60
 Qy 61 EDEETKNNYPRIQCEDGCDPQGLKDNSQCLQRQGAFYKLHLDSDIFKEPALLPDS 120
 Db 61 EDEETKNNYPRIQCEDGCDPQGLKDNSQCLQRQGAFYKLHLDSDIFKEPALLPDS 120
 Qy 121 PMEQLHTSLIGLSQLOPDHPRETOQPSLSSSOORPLRSKLRSLQAFALATAARV 180
 Db 121 PMEQLHTSLIGLSQLOPDHPRETOQPSLSSSQORPLRSKLRSLQAFALATAARV 180
 Qy 181 FAHGAAATTEPPLYTA 196
 Db 181 FAHGAAATTEPPLYTA 196

RESULT 4
 AAB47121
 ID AAB47121 standard; Protein; 196 AA.
 XX
 AC AAB47121;
 XX DT 04-JUN-2001 (first entry)
 DE Murine IL-B30.
 XX Key Location/Qualifiers
 FH 1..21
 FT Peptide /note= "Signal peptide"
 FT Protein 22..196
 FT /note= "Mature protein"
 XX PN WO200118051-A2.
 XX OS Mus musculus.
 XX PD 15-MAR-2001.
 XX PR 08-SEP-2000; 2000WO-US24686.
 XX PR 09-SEP-1999; 99US-0393090.
 PR 10-NOV-1999; 99US-0164616.
 XX PA (SCH) SCHERRING CORP.
 XX PI Oppermann B, De Waal Malefyt R, Rennick DM, Kastlein RA;
 PI Wielkowska MT, Lira SA, Narula SK;
 XX DR WPI: 2001-244560/25.
 DR N-PSDB; AAC85541.

XX Composition comprising interleukin-12 p40 and IL-330 polypeptide or its
 PT segment, useful for ameliorating rheumatoïd arthritis, osteoarthritis,
 PT atherosclerosis, multiple sclerosis, vasculitis and tumour -
 XX Disclosure; Page 11-12; 69PP; English.
 XX
 CC This sequence shows mouse interleukin-B30. Fragments of this protein
 CC may be used in the composition of the invention. The composition
 CC comprises a substantially pure polypeptide comprising a number of
 CC distinct segments of at least 7 contiguous amino acids from IL-12 p40
 CC and/or IL-B30, and a substantially pure polypeptide comprising a
 CC segment of at least 11 contiguous amino acids from IL-12 p40 and/or
 CC IL-B30. The composition is useful for modulating Physiology. Or
 CC development of a cell or tissue in a host organism, resulting in an
 CC increased or decreased production of Interferon-gamma (IFNgamma), an
 CC enhanced Th1 response such as anti-tumour effect, adjuvant effect,
 CC anti-viral effect or antagonized allergic effect, and amelioration
 CC of an autoimmune condition or a chronic inflammatory condition.
 CC IL-B30 or its agonist is useful, inducing the proliferation of memory
 CC T-cells. An agonist or antagonist of IL-B30 protein is useful for
 CC modulating the trafficking or activation of a leukocyte in an animal
 CC experiencing science or symptoms of autoimmunity, an inflammatory
 CC condition, tissue specific autoimmunity, degenerative autoimmunity,
 CC rheumatoïd arthritis, atherosclerosis, multiple
 CC sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a
 CC transplant, spinal injury, stroke, neuroregeneration, an infectious
 CC disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's
 CC disease, postmenopausal osteoporosis or IL-6-associated diseases.

CC IL-12 p40/IL-B30 is useful as an immunogen for the production a
 CC antisera or antibodies specific for binding.
 XX SQ Sequence 196 AA;
 Query Match 100.0%; Score 1038; DB 22; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1. 2e-99;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLDGRAVIMWLWVTPGSSPGLAVPRSSQDWAQQQLSRNCMIAWNHAPGHMNLLREE 60
 Db 1 MLDGRAVIMWLWVTPGSSPGLAVPRSSQDWAQQQLSRNCMIAWNHAPGHMNLLREE 60
 Qy 61 EDEETKNNVPRIODGCDPQGLKDNSQFCLQRGLAFYKHLDDSFIFKEPALPD 120
 Db 61 EDEETKNNVPRIODGCDPQGLKDNSQFCLQRGLAFYKHLDDSFIFKEPALPD 120
 Qy 121 PMEQLHTSLLGLSOLLOPDHPRETQOMPSSLSSQQMORPIJRSKILRSQAFLAAARY 180
 Db 121 PMEQLHTSLLGLSOLLOPDHPRETQOMPSSLSSQQMORPIJRSKILRSQAFLAAARY 180
 Qy 181 FAHGATLTPELVPTA 196
 Db 181 FAHGATLTPELVPTA 196
 RESULT 5
 AAY29783 ID AAY29783 standard; Protein; 189 AA.
 XX AC AAY29783;
 DT 04-NOV-1999 (first entry)
 XX DE Human interleukin B30.
 XX KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
 KW interleukin B30; DCRS1; IL-B30; cytokine receptor; innate immunity;
 KW morphogenic development; immunological disorder.
 OS Homo sapiens.
 XX FH Location/Qualifiers
 FT 1..21
 FT /label= signal
 FT 22..189
 FT /label= IL-B30
 PN WO9940195-A1.
 XX PD 12-AUG-1999.
 XX PF 05-FEB-1999; 99WO-US02600.
 XX PR 13-MAY-1998; 98US-0078194.
 PR 06-FEB-1998; 98US-0073941.
 XX PA (SCHE) SCHERING CORP.
 XX PI Kastellein RA, Mattson JD, McClanahan TK;
 DR WPI; 1999-527306/44.
 XX PT New receptor subunits useful in the treatment inflammatory disorders
 XX PS Claim 2; Page 26-27; 133pp; English.
 XX CC The present invention describes a composition (I) comprising DNAX
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
 CC subunit I (DSRS1) protein, which together encode a new mammalian
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
 CC proteins, or DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1
 CC is useful for screening for ligands (i.e. agonists/antagonists) from
 CC a library of compounds which are useful for modulating the physiology
 CC or development of a cell or tissue culture e.g. inflammatory responses,
 CC immune and/or morphogenic development. (R), antibodies and
 CC ligands are useful for treatment of conditions, especially immunological
 CC disorders, associated with conditions exhibiting abnormal expression of
 CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,
 CC and the subunits DRS1 and DCRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and
 CC variants from other individuals or species. The present sequence
 CC represents the specifically claimed human IL-B30, for use in the
 CC composition of the present invention.
 XX SQ Sequence 189 AA;
 Query Match 69.2%; Score 718.5; DB 20; Length 189;
 Best Local Similarity 74.6%; Pred. No. 1. 8e-66;
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps
 Qy 1 MLDGRAVIMWLWVTPGSSPGLAVPRSSQDWAQQQLSRNCMIAWNHAPGHMNLLREE 60
 Db 1 MLGSRAVMLLPLPTAQGRAVPGSSPAVTOCQLSKQCTILAWSAHPVGHMD-LBEE 59
 Qy 61 EDEETKNNVPRIODGCDPQGLKDNSQFCLQRGLAFYKHLDDSFIFKEPALPD 120
 Db 60 GDEETINDVPHIQCSDGCDFOGLRNSQFLQRLTHQGLIFYEKUQSLDTFGEPSLLIDS 119
 Qy 121 PMEQLHTSLLGLSOLLOPDHPRETQOMPSSLSSQQMORPIJRSKILRSQAFLAAARY 180
 Db 120 PVAQHLASLGLSQLQIPGEHHWTQIPSLSPQWPWLRFLRKILRSQAFVAAARY 179
 RESULT 6
 AAW95002 ID AAW95002 standard; Protein; 189 AA.
 XX AC AAW95002;
 XX DT 21 MAY 1999 (first entry)
 XX DE Human interleukin-B30 (IL-B30) polypeptide.
 XX KW Cytokine; interleukin B30; IL-B30; forensic science; cell proliferatio
 KW inflammatory condition; drug screening; human.
 XX OS Homo sapiens.
 XX FH Location/Qualifiers
 FT Key
 FT Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..189
 FT /note= "mature protein"
 XX PN WO9905260-A1.
 XX PD 04-FEB-1999.
 XX PR 25-JUL-1997; 97US-0900905.
 XX PA (SCHE) SCHERING CORP.
 XX PT Bazar JF;
 XX DR WPI; 1999-142935/12.
 DR N-PSDB; AAX17786.

XX Newly isolated or recombinant polynucleotide encoding mammalian PT cytokine interleukin-B30 (IL-B30), including fragments - useful for PT regulating activation, development, differentiation and function of PT various cell types, and for diagnosing and treating conditions XX associated with IL-B30

PS Claim 2; Page 8-9; 83pp; English.

XX This represents a human cytokine interleukin-B30 (IL-B30) polypeptide. CC Host cells containing a vector comprising the IL-B30 nucleic acid are CC used for the recombinant production of the protein. The polynucleotides CC are useful for diagnosis of IL-B30 mediated conditions, and forensic CC science (e.g. to distinguish rodent from human, or as a marker to CC distinguish between different cells exhibiting differential expression or CC modification patterns). The IL-B30 (including fragments), together with CC antibodies that bind to IL-B30 are useful for teaching purposes. They CC are also used for treating conditions associated with abnormal physiology CC or development, including inflammatory conditions. The polypeptide CC cytokine should mediate cytokine synthesis and proliferation in cells. CC IL-B30 is useful for drug screening to identify compounds having binding CC affinity to IL-B30.

XX Sequence 189 AA;

Query	Match	Score	Length
Best Local Similarity	69.2%	DB 20;	189;
Matches 141; Conservative	74.6%;	Pred. No. 1.8e-66;	
Mismatches 14;	Indels 33;	Gaps 1;	

Qy 1 MLDGRAVIMLWLLPWTTQGLAVPRSSPDNAQCQQLSRNLCAWNAAHAPAGHMNLLREDE 60
Db 1 MUGSRMVLMLLWLLPWTAQGRAVPGGSSPAWTCQQQLSQQKLCTLAWSAHPLVGHMD-LRDE 59

Qy 61 EDEBETANVPRIQEDCDPGLKNSQFCLQRGAFYKHLDSDFEKGEPAALLPS 120
Db 60 GDEBETNDVPHIQCGDQGLDRNSQFCIQRTHQGLFYKEKLGSDFTGEPSLLPS 119

Qy 121 PMEQLHTSLIGLSQIQLQPEDHPRETOQMPSSQWORPLRSKILRSQAFIAARY 180
Db 120 PVAQLIASLIGLSQIQLQPEGHHWETOQIPSPQWQRLRFKILRSQAFAVAARY 179

Qy 181 FAHGAATL 189
Db 180 FAHGAATLS 188

RESULT 7
ID AAB01981
XX Human interleukin-B30 (IL-B30).
XX DT 27-SEP-2000 (first entry)
XX DE Human
XX FT Location/Qualifiers
PT 1..21
FT /note= "Signal peptide"
Protein
FT 22..189
FT /note= "Mature human IL-B30"
XX OS Homo sapiens.
XX FH Key
Peptide
FT Location/Qualifiers
PT 1..21
FT /note= "Signal peptide"
Protein
FT 22..189
FT /note= "Mature human IL-B30"
XX PN US6060284-A.
XX PD 09-MAY-2000.
XX

PP 24-JUL-1998; 98US-0122443.
XX PR 25-JUL-1997; 97US-0053765.
XX PA (SCHE) SCHERING CORP.
XX PT Bazan JF;
XX DR WPI; 2000-364420/31.
DR N-PSDB; AAA52574.

XX Novel recombinant DNA encoding cytokines especially interleukin-B30 PT useful as probes or primers for diagnosing immune disorders including PT autoimmune or chronic inflammatory conditions -

XX PS Claim 1; Column 5-8; 32pp; English.

CC This sequence represents human interleukin-B30 (IL-B30). IL-B30 is a novel cytokine, exhibiting significant homology to IL-6 and GCSF (granulocyte colony stimulating factor). Cytokines play a critical role in signalling between immune or other cells during an immune response. The precise role if IL-B30 is not yet known - it is likely to have either a stimulatory or an inhibitory effect on haematopoietic cells such as T-cells, B-cells, natural killer (NK) cells and macrophages.

CC Alternatively, it may affect vascular physiology or development, or have neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and antagonists are useful in the diagnosis and treatment of disorders associated with abnormal expression or activity of IL-B30 e.g., inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are useful for recombinant expression of IL-B30 in a host cell, and as a source of probes and primers. The IL-B30 probes and primers can be used to detect levels of IL-B30 expression in samples from patients suspected of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may also be used to identify homologous genes in other species. IL-B30 protein or its fragments are useful as antigens for raising antibodies to various linear and conformational epitopes. Such antibodies may be used to detect levels of IL-B30 protein in a sample.

XX Sequence 189 AA;

Qy 1 MLDGRAVIMLWLLPWTTQGLAVPRSSPDNAQCQQLSRNLCAWNAAHAPAGHMNLLREDE 60
Db 1 MUGSRMVLMLLWLLPWTAQGRAVPGGSSPAWTCQQQLSQQKLCTLAWSAHPLVGHMD-LRDE 59

Qy 61 EDEBETANVPRIQEDCDPGLKNSQFCLQRGAFYKHLDSDFEKGEPAALLPS 120
Db 60 GDEBETNDVPHIQCGDQGLDRNSQFCIQRTHQGLFYKEKLGSDFTGEPSLLPS 119

Qy 121 PMEQLHTSLIGLSQIQLQPEDHPRETOQMPSSQWORPLRSKILRSQAFIAARY 180
Db 120 PVAQLIASLIGLSQIQLQPEGHHWETOQIPSPQWQRLRFKILRSQAFAVAARY 179

Qy 181 FAHGAATL 189
Db 180 FAHGAATLS 188

Qy 1 MLDGRAVIMLWLLPWTTQGLAVPRSSPDNAQCQQLSRNLCAWNAAHAPAGHMNLLREDE 60
Db 1 MUGSRMVLMLLWLLPWTAQGRAVPGGSSPAWTCQQQLSQQKLCTLAWSAHPLVGHMD-LRDE 59

Qy 61 EDEBETANVPRIQEDCDPGLKNSQFCLQRGAFYKHLDSDFEKGEPAALLPS 120
Db 60 GDEBETNDVPHIQCGDQGLDRNSQFCIQRTHQGLFYKEKLGSDFTGEPSLLPS 119

Qy 121 PMEQLHTSLIGLSQIQLQPEDHPRETOQMPSSQWORPLRSKILRSQAFIAARY 180
Db 120 PVAQLIASLIGLSQIQLQPEGHHWETOQIPSPQWQRLRFKILRSQAFAVAARY 179

Qy 181 FAHGAATL 189
Db 180 FAHGAATLS 188

RESULT 8
ID AAB47120 standard; Protein; 189 AA.
XX AC AAB47120;
XX DT 04-JUN-2001 (first entry)
XX DE Human IL-B30.
XX KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma; IFNgamma; Th1 response; autoimmune disease; chronic inflammation;

for treating, preventing or ameliorating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunodeficiency ('SCID'), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus ('HIV'), hepatitis, herpesviruses, mycobacteria, leishmania spp., malaria and erythematous, rheumatoid arthritis, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host-disease and autoimmune inflammatory eye disease. The proteins can also be used to treat allergic conditions, such as asthma. AA16658 to AA16774 represent probes for the human secreted proteins from the present invention.

Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;

Best Local Similarity 74.6%; Pred. No. 2.3e-66;

Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

XX 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60

XX 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Db 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120

Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 61 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180

Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180

Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189

Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;
Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60
Db 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Qy 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120
Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180
Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189
Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;
Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60
Db 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Qy 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120
Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180
Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189
Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;
Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60
Db 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Qy 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120
Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180
Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189
Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;
Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60
Db 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Qy 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120
Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180
Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189
Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;
Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60
Db 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Qy 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120
Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180
Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189
Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;
Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLDCRAVIMWLLPWTQGLAVPRSSSPDWAQCQQLSRNLCMLAMNAHAAPAGHNNLREE 60
Db 1 MLGSRAVMWLLLPWTQGRAYPGGSSPAWTOCQQLSKLCTLAWAHLVGHMD-LREE 59

Qy 61 EDEETKVNVPRIQEDCDPGLKDNQSCLQRIGLAFYKHLDSDFKGERALLPDS 120
Db 60 GDEETTNYPHQCGCDPGLDRNSQCLQRIGLTYEKULGSDFTGEPSLPLPS 119

Qy 121 PMEQLHTSLLGSLQQLLOPEDHPRETOOMPSLSSQQWQPLRSKILRSIQAFLIAARY 180
Db 120 PVGQLHASLGLSQQLQPEGHMETQIPSLSPSQPRQRLLRFKILRSIQAFLIAARY 179

Qy 181 FAHGAATLT 189
Db 180 FAHGAATLS 188

RESULT 11
AAU12287

ID AAU12287 standard; Protein; 189 AA.
XX
AC AAU12287;
XX
DT 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX PN WO200140466-A2.

XX PD 07-JUN-2001.

XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28624.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US1243.

PR 06-JAN-2000; 2000WO-US0277.

PR 06-JAN-2000; 2000WO-US0376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PT in immune and haematopoiesis systems -
XX
PS Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
CC family. The protein can be used in drugs for treating diseases due to
CC abnormality of cell proliferation in the immune system and haematopoietic
CC system.

XX SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;
Best Local Similarity 74.6%; Pred. No. 2.3e-66;

PR	24-FEB-2000; 2000WO-US05004.	ID AAB48070 standard; protein; 189 AA.
PR	01-MAR-2000; 2000WO-US05601.	XX
PR	20-MAR-2000; 2000WO-US07377.	AC
PR	21-MAR-2000; 2000WO-US07532.	XX
PR	30-MAR-2000; 2000WO-US08439.	DT 19-MAR-2001 (first entry)
PR	17-MAY-2000; 2000WO-US13705.	XX
PR	22-MAY-2000; 2000WO-US14042.	DE
PR	30-MAY-2000; 2000WO-US14941.	XX
PR	02-JUN-2000; 2000WO-US15264.	KW
PR	10-NVY-2000; 2000WO-US30873.	KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal; virucide; antibacterial; anti-HIV; human immunodeficiency virus;
XX		KW anticonvulsant; cerebroprotective; nootropic; antiulcer; antifungal; KW antinfertility; tranquilizer; neuroleptic; vasotropic; gynecological; KW keratolytic; protozoicide; gene therapy.
PA	(GETH) GENENTECH INC.	XX
PI	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	XX
PI	Gerritsen ME, Goddard A, Gurney AL, Sherwood S;	OS
PI	Smith V, Stewart TA, Tumas D, Watanabe CR, Wood WI, Zhang Z;	XX
XX		Homo sapiens .
DR	WPI; 2001-408201/43.	PN WO200070049-A2.
DR	N-PSDB; AAS2139.	PD 23-NOV-2000.
XX		XX
PT	Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PT PRO polypeptides, and detect the presence of mammalian tumours e.g. PT lung, breast, prostate, cervical -	XX
PT	XX	XX
PS	Claim 12; Fig 232; 813pp; English.	XX
XX		XX
CC	AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical, or liver tumours by comparing PRO polypeptide expression in cell sample to that in a control sample.	XX
CC	Some of the 275 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC cartilage, the proliferation of inner ear atricular supporting cells or CC T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of CC the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polynucleotides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.	XX
XX		XX
SQ	Sequence 189 AA;	1;
	Query Match Similarity 69.1%; Score 717.5; DB 22; Length 189;	
	Best Local Similarity 74.6%; Pred. No. 2.3e-66;	
	Matches 14; Conservative 14; Mismatches 33; Indels 1; Gaps 1;	
QY	1 MLDCAVTLWLLPWTQGLAVPRSSSPDQGKLNQFCQLTQGLATYKHLDSDFIKGEPALPDSD 60	
Db	1 MIGSRAYMLLWLLPWTQGLAVPRSSSPDQGKLNQFCQLTQGLATYKHLDSDFIKGEPALPDSD 59	
QY	61 EDEETKNNVPRTCEDGCDPQGLKNSQFCQLTQGLATYKHLDSDFIKGEPALPDSD 120	
Db	60 GDEETTNDVPHIQQCGDCDPQGLRDNQFCQLTQGLATYKHLDSDFIKGEPALPDSD 119	
QY	121 PMEQLHTSLGLSQLQPEDIPRETPQMPSELSQOWQRLRSKTLRSQAFALATAARY 180	
Db	120 PVQLHSLGLSQLQPEGHHWETQOPLSPSQWLRLRFKILRSQAFVAVAARY 179	
QY	181 FAHGAAIT 189	
Db	180 FAHGAAIT 188	

XX Sequence 189 AA;
 XX Query Match 69.1%; Score 717.5; DB 22; Length 189;
 CC Best Local Similarity 74.6%; Pred. No. 2.3e-66;
 CC Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 0;
 CC
 CC represents the partial pig IL-B30, given in the present invention.
 XX SQ Sequence 102 AA;

QY 1 MLDICRAVIMLWLPWVTPGLAVPRSSSPDWAQCOOLSRNCLMIAWNAAHAPAGHMNLRE 60
 DB 1 MGSRAYMLLILPWTAAQGRVPGSSSPAWTOCQLSQRKLTAWSAHPFLVGHMID-LRE 59
 QY 61 EDEBETKNNVPRIOCEDGCDPGKLKDNSQFCIQRQGLAFYKHLLSDTIEKGEPALLPS 120
 DB 60 GDEETINNDVPHIQCGDCPDGLRDNQFCIQRQGLFYKEKLGSDFITGEPSLIPDS 119
 QY 121 PHEQLHTSSLGTSQQLQPEPDIPRETOQMPSSQWQPLREKTLRSQFLATIARY 180
 DB 120 PGQLHASSLGTSQQLQPEGHWTQQIPSLSPSWPQRLRLLRFKILRSQFLAVAVARV 179
 QY 181 FAHGAATLT 189
 DB 180 FAHGAATLS 188

RESULT 1.3
 ID AA29787 standard; Protein; 102 AA.
 XX AA29787;
 XX DT 04-NOV-1999 (first entry)
 XX DE Partial pig interleukin B30 protein.
 XX KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
 XX interleukin B30; DRS1; DCRS1; IL-B30; cytokine receptor; diagnosis;
 XX inflammatory disorder; inflammatory response; innate immunity;
 XX morphogenic development; immunological disorder.
 XX OS Sus scrofa.
 XX PN WO940195-A1.
 XX PD 12-AUG-1999.
 XX PP 05-FEB-1999; 98WO-US02600.
 XX PR 13-MAY-1998; 98US-0078194.
 XX PR 06-FEB-1998; 98US-0073941.
 XX PA (SCHE) SCHERING CORP.
 XX PI Kastelein RA, Mattson JD, McClanahan TK;
 XX DR WPI; 1999-527306/44.
 XX PT New receptor subunits useful in the treatment inflammatory disorders
 XX Disclosure; Page 29; 133pp; English.
 XX
 CC The present invention describes a composition (I) comprising DNAX
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
 CC subunit I (DSRS1) protein, which together encode a new mammalian
 CC cytokine related receptor (R), or DRS1 and interleukin B30 (IL-B30)
 CC proteins, or DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1
 CC is useful for screening for ligands (i.e. agonists/antagonists) from
 CC a library of compounds, which are useful for modulating the physiology
 CC or development of a cell or tissue culture e.g. inflammatory responses,
 CC innate immunity and/or morphogenic development. (R), antibodies and
 CC ligands are useful for treatment of conditions, especially immunological
 CC disorders, associated with conditions exhibiting abnormal expression of
 CC (R). (R) is useful as a phospho labeling enzyme to label substrates,
 CC and the subunits DRS1 and DCRS1 are useful as immunogens for generating
 CC sequence represents a pig IL-B30.
 XX SQ Sequence 102 AA;

CC antibodies, or as antigens for binding antibodies. Nucleic acids
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and
 CC variants from other individuals or species. The present sequence
 CC represents the partial pig IL-B30, given in the present invention.
 XX SQ Sequence 102 AA;

Query Match 34.3%; Score 356; DB 20; Length 102;
 CC Best Local Similarity 72.3%; Pred. No. 3.8e-29;
 CC Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps 0;
 CC
 QY 90 CLQRHQGLAFYKHLLSDTIEKGEPALLPSMEQLHTSSLGTSQQLQPEPDIPRETOQMP 149
 DB 2 CLQRHQGLFYKEKLGSDFITGEPSLIPDSLQHDSLGLRQLQPEGHHWEIQTP 61
 QY 150 SLSSSQWQPLRPLREKTLRSQFLAFTAIAARVFVAHGAATTE 190
 DB 62 SPSPSPWPQRLRLLRFKILRSQFLAVAVARVFAHGAATLSQ 102

RESULT 14
 ID AAW95004 standard; peptide; 102 AA.
 XX AAW95004;
 XX AC AAW95004;
 XX DT 21-MAY-1999 (first entry)
 XX DE Pig interleukin-B30 (IL-B30) polypeptide.
 XX KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
 XX KW inflammatory condition; drug screening; pig.
 XX OS Sus scrofa.
 XX PN WO9905280-A1.
 XX PD 04-FEB-1999.
 XX PF 24-JUL-1998; 98WO-US15423.
 XX PR 25-JUL-1997; 97US-0900905.
 XX PA (SCHE) SCHERING CORP.
 XX PI Buzan JF;
 XX DR WPI; 1999-142935/12.

PT Newly isolated or recombinant polynucleotide encoding mammalian
 PT cytokine interleukin B30 (IL-B30), including fragments - useful for
 PT regulating activation, development, differentiation and function of
 PT various cell types, and for diagnosing and treating conditions
 PT associated with IL-B30
 XX Claim 1; Page 11-12; 83pp; English.
 XX This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
 CC polypeptides. Host cells containing a vector comprising the IL-B30
 CC nucleic acids are used for the recombinant production of the proteins.
 CC The polynucleotides are useful for diagnosis of IL-B30 mediated
 CC conditions, and forensic science (e.g. to distinguish rodent from human
 CC or as a marker to distinguish between different cells exhibiting
 CC differential expression or modification patterns). The IL-B30 (including
 CC fragments), together with antibodies that bind to IL-B30 are useful for
 CC teaching purposes. They are also used for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions. The polypeptide cytokine should mediate cytokine synthesis
 CC and proliferation in cells. IL-B30 is useful for drug screening to
 CC identify compounds having binding affinity to IL-B30. The present
 CC sequence represents a pig IL-B30.
 XX SQ Sequence 102 AA;

RESULT 15
 AAB01983 standard; Protein; 102 AA.
 ID XX
 AC AAB01983;
 XX DT 27-SEP-2000 (first entry)
 DE Mature porcine interleukin-B30 (IL-B30).
 XX KW IntesLeukin-B30; IL-B30; porcine; Pig; cytokine; cellular signalling;
 KW immune response; haematopoietic cell; IL-6 homologue; G-CSF homologue;
 KW granulocyte colony stimulating factor; immune disorder; antibody.
 KW inflammatory disease; autoimmune disease; antigen; antibody.
 XX OS Sus scrofa.
 XX PN US6060284 A.
 XX PD 09-MAY-2000.
 XX PF 24-JUL-1998; 98US-0122443.
 XX PR 25-JUL-1997; 97US-0053765.
 XX PA (SCHHE) SCHERING CORP.
 PI Bazan JF;
 XX DR WPI; 2000-364420/31.
 XX PT Novel recombinant DNA encoding cytokines especially interleukin-B30
 PT useful as probes or primers for diagnosing immune disorders including
 PT autoimmune or chronic inflammatory conditions -
 XX PS Claim 1; Column 45-46; 32pp; English.
 XX CC This sequence represents porcine interleukin-B30 (IL-B30). IL-B30
 CC is a novel cytokine, exhibiting significant homology to IL-6 and
 CC G-CSF (granulocyte colony stimulating factor). Cytokines play a critical
 CC role in signalling between immune or other cells during an immune
 CC response. The precise role if IL-B30 is not yet known - it is likely to
 CC have either a stimulatory or an inhibitory effect on haematopoietic cells
 CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.
 CC Alternatively, it may affect vascular physiology or development, or have
 CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and
 CC antagonists are useful in the diagnosis and treatment of disorders
 CC associated with abnormal expression or activity of IL-B30 e.g.,
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are
 CC useful for recombinant expression of IL-B30 in a host cell, and as a
 CC source of probes and primers. The IL-B30 probes and primers can be used
 CC to detect levels of IL-B30 expression in samples from patients suspected
 CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may
 CC also be used to identify homologous genes in other species. IL-B30
 CC protein or its fragments are useful as antigens for raising antibodies to
 CC various linear and conformational epitopes. Such antibodies may be used
 CC to detect levels of IL-B30 protein in a sample.
 SQ Sequence* 102 AA;

Search completed: November 20, 2002, 11:53:01
 Job time : 35.6 secs

Query Match	Score 356;	DB 20;	Length 102;	Score 34.3%;	DB 21;	Length 102;	
Best Local Similarity	72.3%;	Pred. No.	3.0e-29;	Best Local Similarity	72.3%;	Pred. No.	3.8e-29;
Matches 73;	Conservative 8;	Mismatches 20;	Indels 0;	Matches 73;	Conservative 8;	Mismatches 20;	Indels 0;
Gaps 0;				Gaps 0;			
Qy 90 CLQRIGLAFYKLDSDFIKGEPALLPSMEQLHSLGLSQLQPEDHPRETQOMP 149				Qy 90 CLQRIGLAFYKLDSDFIKGEPALLPSMEQLHSLGLSQLQPEDHPRETQOMP 149			
Db 2 CLQRIGLAFYKLGSDFITGEPSLHPDGSVQLHASLGLRQLQPECHHWETEQTP 61				Db 2 CLQRIGLAFYKLGSDFITGEPSLHPDGSVQLHASLGLRQLQPECHHWETEQTP 61			
Qy 150 SLSQQWQPPLRSKILRSQAFLATAARVFAHGAATLIE 190				Qy 150 SLSQQWQPPLRSKILRSQAFLATAARVFAHGAATLIE 190			
Db 62 SPSPSQWPQLRLKTRSLQAFVAAARVFAHGAATLSQ 102				Db 62 SPSPSQWPQLRLKTRSLQAFVAAARVFAHGAATLSQ 102			

OM protein - protein search, using sw model
 Copyright (c) 1993 - 2002 Compugen Ltd.
 Run on: November 20, 2002, 11:54:30 ; Search time 7 63636 Seconds
 (without alignments)
 401.978 Million cell updates/sec
 Title: US-09-658-699-4
 Perfect score: 1038
 Sequence: 1 MLDRAVIMLWLPWTQGL.....AARVFAHGAAATLEPLVPTA 196
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 100480 seqs, 15661496 residues
 Total number of hits satisfying chosen parameters: 100480
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 List Inc first 15 summarization
 List Inc first 15 summarization

Database 1 1 1 1 1 1 1 1

ALIGNMENTS

```

Published Applications AA: *
1: /cgn2_6/picodata/1/pubpaa/1
2: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
3: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
4: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
5: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
6: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
7: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
8: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
9: /cgn2_6/picodata/1/pubpaa/1/pubpaa/P
10: /cgn2_6/picodata/1/pubpaa/1/pubpaa/
11: /cgn2_6/picodata/1/pubpaa/1/pubpaa/
12: /cgn2_6/picodata/1/pubpaa/1/pubpaa/
13: /cgn2_6/picodata/1/pubpaa/1/pubpaa/
14: /cgn2_6/picodata/1/pubpaa/1/pubpaa/

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	88	8.5	181	10	US-09-764-864-1144
2	88	8.5	181	10	US-09-764-864-1159
3	84	8.1	212	10	US-09-854-280-14
4	84	8.1	212	10	US-09-854-208-14
5	81.5	7.9	175	10	US-09-854-332-80
6	79.5	7.7	175	10	US-09-754-532-79
7	78.5	7.6	175	10	US-09-754-532-92
8	78.5	7.6	175	10	US-09-754-532-106
9	78.5	7.6	175	10	US-09-754-532-109
10	78	7.5	285	10	US-09-815-242-5068
11	77.5	7.5	348	12	US-10-003-496-6
12	76.5	7.4	174	10	US-09-760-008A-1
13	76	7.4	174	10	US-09-950-473-2
14	76.5	7.4	174	12	US-10-016-403-2
15	76.5	7.4	174	12	US-10-016-403-3
16	76.5	7.4	174	12	US-10-003-496-1
17	76.5	7.4	174	12	US-09-754-532-67
18	76.5	7.4	175	10	US-09-754-532-67
19	76.5	7.4	175	10	US-09-754-532-67

20	7.4	175	10	US-09-754-532-68	Sequence 68, App1
21	7.4	175	10	US-09-754-532-69	Sequence 69, App1
22	7.4	175	10	US-09-754-532-70	Sequence 70, App1
23	7.4	175	10	US-09-754-532-71	Sequence 71, App1
24	7.4	175	10	US-09-754-532-72	Sequence 72, App1
25	7.4	175	10	US-09-754-532-73	Sequence 73, App1
26	7.4	175	10	US-09-754-532-74	Sequence 74, App1
27	7.4	175	10	US-09-754-532-75	Sequence 75, App1
28	7.4	175	10	US-09-754-532-76	Sequence 76, App1
29	7.4	175	10	US-09-754-532-77	Sequence 77, App1
30	7.4	175	10	US-09-754-532-78	Sequence 78, App1
31	7.4	175	10	US-09-754-532-83	Sequence 83, App1
32	7.4	175	10	US-09-754-532-84	Sequence 84, App1
33	7.4	175	10	US-09-754-532-85	Sequence 85, App1
34	7.4	175	10	US-09-754-532-86	Sequence 86, App1
35	7.4	175	10	US-09-754-532-87	Sequence 87, App1
36	7.4	175	10	US-09-754-532-88	Sequence 88, App1
37	7.4	175	10	US-09-754-532-89	Sequence 89, App1
38	7.4	175	10	US-09-754-532-94	Sequence 94, App1
39	7.4	175	10	US-09-754-532-95	Sequence 95, App1
40	7.4	175	10	US-09-754-532-96	Sequence 96, App1
41	7.4	175	10	US-09-754-532-97	Sequence 97, App1
42	7.4	175	10	US-09-754-532-99	Sequence 99, App1
43	7.4	175	10	US-09-754-532-100	Sequence 100, App1
44	7.4	175	10	US-09-754-532-101	Sequence 101, App1
45	7.4	175	10	US-09-754-532-102	Sequence 102, App1

RESULT 1
US-09-764-864-1144
; Sequence 1144, Application US/09764864
; Patent No. US20020132753A1

Sequence 1559, Application US/09764864
; Patient No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764, 864
; CURRENT FILING DATE: 2001-01-17
; prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1559
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-1559

Query Match 8.5%; Score 88; DB 10; Length 181;
Best Local Similarity 23.7%; Pred. No. 0.057; Mismatches 50; Indels 82; Gaps 11;

Db 8 WLLPKPKPSGICLGTWAPGSSHWACOGL-----WGAGPA----- 45

Qy 11 WLFWWTGGLAVRSPSS---DWAQCOQLSRNLCMLAWNHA-PAGHMNLREEEDEET 65

Db 46 -----TGSOPIGKEDCDPOGLKDNSOFCLQRIRQGL-----AFYKHLDS-DIF 110

Qy 66 KNNVPRIQCEGDCDPOGLKDNSOFCLQRIRQGL----- 45

Db 46 -----TGSOPIGKEDCDPOGLKDNSOFCLQRIRQGL-----AFYKHLDS-DIF 110

Qy 111 KGEPAL---LPDSPMEQHLSLQLQDHPRETQMPSSSSQQWQP---- 160

Db 90 GGHSVAGYWEPFLSSHPFSMGCL-----PR-SRSPSSPSPQWKPVDTA 139

Qy 161 ---LLRSKLRSQAFL 174

Db 140 VGGRLCKSLTGFAGLEGFL 157

RESULT 3
US-09-854 280-14
; Sequence 14, Application US/09854280
; Patient No. US20020052027A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C2
; CURRENT APPLICATION NUMBER: US/09/854, 280
; CURRENT FILING DATE: 2001-05-10
; prior application number: US 09/311, 832
; prior filing date: 1998-05-14
; prior application number: US 60/085, 579
; prior filing date: 1998-12-23
; SEQ ID NO 14
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-280-14

Query Match 8.1%; Score 84; DB 10; Length 212;
Best Local Similarity 21.5%; Pred. No. 0.19; Mismatches 28; Indels 40; Gaps 7;

Db 59 YILDGISALRKET-----CNK-SNMCESSKEALA----- 74

Qy 15 WTQGLAVPSSSPDWAOQQLSRNLCMLAWNHA-PAGHMNLREEEDEETRNVPRIQC 74

Db 59 YILDGISALRKET-----CNK-SNMCESSKEALA-----ENNLNPKMAE 97

Qy 133 SQLQPE-----DHPREQMPSSSSQWQRLRSKILRSQAFLAIAAR 179

Db 151 IQFLOKAKNLDATTPDPTTNASLLTKLQAQNOWLQDMTHLILRSKEFLOSSLR 207

RESULT 4
US-09-854-208-14
; Sequence 14, Application US/09854208
; Patient No. US20020106743A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1
; CURRENT APPLICATION NUMBER: US/09/854, 208
; prior application number: US 60/311, 832
; prior filing date: 1999-05-14
; prior application number: US 60/085, 579
; prior filing date: 1998-12-23
; SEQ ID NO 14
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-208-14

Query Match 8.1%; Score 84; DB 10; Length 212;
Best Local Similarity 21.5%; Pred. No. 0.19; Mismatches 28; Indels 40; Gaps 7;

Db 59 YILDGISALRKET-----CNK-SNMCESSKEALA----- 74

Qy 15 WTQGLAVPSSSPDWAOQQLSRNLCMLAWNHA-PAGHMNLREEEDEETRNVPRIQC 74

Db 59 YILDGISALRKET-----CNK-SNMCESSKEALA-----ENNLNPKMAE 97

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/754,532
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/448,716
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-754-532-80

Query Match 7.9%; Score 81.5; DB 10; Length 175;
Best Local Similarity 30.4%; Pred. No. 0.26; Mismatches 36; Indels 27; Gaps 7;
Matches 35; Conservative 17; Number of Sequences: 110

QY 90 CLQRIRGGLAFYKHLDSDFIKG -EPALLPDSPMQLHTS ------LIGLSQLQ 137
Db 75 CLSQLHSGLFLYQGLQA --LEGISPELGPTLDTQLDVADEFATIWOQMEELGMAPALQ 132

QY 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRSQAFIAARYFAHGA 186
Db 133 P-----TQGAMPAPASA -FQRAGGVLYASHLQSLEVSYRVLHAA 174

RESULT 7
US-09-754-532-92
Sequence 92, Application US/09/754532
Patent No. US20010016191A1
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
ZIP: 91320-1789
COUNTRY: United States of America

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/754,532
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/448,716
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-8011
TELEFAX: 805/499-5725
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-754-532-92

Query Match 7.6%; Score 78.5; DB 10; Length 175;
Best Local Similarity 30.4%; Pred. No. 0.54; Mismatches 37; Indels 27; Gaps 7;
Matches 35; Conservative 16; Number of Sequences: 110

QY 90 CLQRIRGGLAFYKHLDSDFIKG -EPALLPDSPMQLHTS ------LIGLSQLQ 137
Db 75 CLSQLHSGLFLYQGLQA --LEGISPELGPTLDTQLDVADEFATIWOQMEELGMAPALQ 132

QY 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRSQAFIAARYFAHGA 191
Db 133 P-----TQGAMPAPASA -FQRAGGVLYASHLQSLEVSYRVLH--LAQP 175

RESULT 8

US-09-754-532-106
; Sequence 106, Application US/09754532
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754, 532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448, 716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 9
US-09-754-532-109
; Sequence 109, Application US/09754532
; Patent No. US/00016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754, 532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448, 716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-109

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 10
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haselbeck, Robert
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 11
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ohlsen, Karl L.
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 12
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zyskind, Judith W.
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 13
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wall, Daniel
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 14
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trawick, John D.
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 15
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carr, Grant J.
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 16
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Yamamoto, Robert T.
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 17
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Xu, H. Howard
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 18
US-09-115-242-5068
; Sequence 5068, Application US/09815242
; Patent No. US/0020061563A1
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haselbeck, Robert
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-106

Query Match 7.6%; Score 78.5%; DB 10; Length 175;
Best Local Similarity 29.6%; Pred. No. 0.54;
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

Qy 90 CLQRTRQGLAFYKHLDSDIFKG-EPALLPDSPMEQLHTS-----LLGSQLIQ 137
Db 75 CLSQLHSGLFLYGLIQA--LEGISPELGTPLDTLQLDVAFAFTTINQMEALGMAPLQ 132
Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKLRLSLOAFLATAARVFAHGAATLTP 191
Db 133 P-----TQGAMPAPASA-FQRAGGVLYVASHLQSFLVEVSYRLRH---LAQP 175

RESULT 19
US-09-754-532-109
; Sequence 109, Application US/09754532
; Patent No. US/00016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match 7.5%; Score 78; DB 10; Length 285;
 Best Local Similarity 24.2%; Pred. No. 1.2; Mismatches 71; Indels 46; Gaps 9;
 Matches 45; Conservative 24; Mismatches 24;

Qy 45 WNAHAPAGHMNLIREEDEETKNNVPR-----TQCEDGCDPGLKDNSQFCIQR-R 93
 Db 51 WLAQAVDHLRLLEVEPEQSSETTLRLLNDIQQDRWAQDPAACSLLR 110

Qy 94 IROGLAFYKHLDSDFK-GEPALPDSPMEQL-HITULLGSQLQPEDHP---- 142
 Db 111 IRGEIELNIGDSRILQVRSGVRSFGLAHFCRM--REEHQPWDHAE 168

Qy 143 -----RETQOMP---SLSQQWQPLRSKIL-TRSQFLAIAARYFAHGA 185
 Db 169 LFKAASRPPVRQRNLLMKNPEGYWALDISRNLGQVQRETULPLAALRSFV----LMTDGF 223

Qy 186 ATLTEP 191
 Db 224 DRIVEP 229

RESULT 11
 US-10-003-496-6
 ; Sequence 6, Application US/10003496
 ; Patent No. US2002014296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maxygen ApS
 ; TITLE OF INVENTION: Single-Chain Polypeptides
 ; FILE REFERENCE: 0218us210
 ; CURRENT APPLICATION NUMBER: US10/003,496
 ; CURRENT FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/245,727
 ; PRIOR FILING DATE: 2000-11-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 6
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Single chain G-CSF dimer polypeptide
 US-10-003-496-6

Query Match 7.5%; Score 77.5; DB 12; Length 348;
 Best Local Similarity 30.0%; Pred. No. 1.8; Mismatches 17; Indels 25; Gaps 7;
 Matches 36; Conservative 17; Mismatches 17;

Qy 90 CLQRIRGAFYKHLDSDFK-GEPALPDSPMEQLHTS-----LLGSQLQ 137
 Db 74 CLSQHSGLFLYQGLQA--LEGISPEGLPTLDLQDADFTTIWQMEELGMAPAQ 131

Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKIL-TRSQFLAIAARYFAHGAITLEPLVTA 196
 Db 132 P-----TQGAMPAPASA--FQRAGGVLYASHLQSFLEVSYRLRH----LAQP 174

RESULT 12
 US-09-760-008A-1
 ; Sequence 1, Application US/09760008A
 ; Patent No. US200200443A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NISSEN, TORBEN LAUSSAARD
 ; APPLICANT: ANDERSEN, KIM VILBOUR
 ; APPLICANT: HANSEN, CHRISTIAN KARSTEN
 ; APPLICANT: MIKKELSEN, JAN MOLLER
 ; TITLE OF INVENTION: G-CSF CONJUGATES
 ; FILE REFERENCE: 31-000700US
 ; CURRENT APPLICATION NUMBER: US/09/760,008A
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/176,376
 ; PRIOR FILING DATE: 2000-01-14

Query Match 7.4%; Score 76.5; DB 10; Length 174;
 Best Local Similarity 29.6%; Pred. No. 0.86; Mismatches 17; Indels 27; Gaps 7;
 Matches 34; Conservative 17; Mismatches 17;

Qy 90 CLQRIRGAFYKHLDSDFK-GEPALPDSPMEQLHTS-----LLGSQLQ 137
 Db 74 CLSQHSGLFLYQGLQA--LEGISPEGLPTLDLQDADFTTIWQMEELGMAPAQ 131

Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKIL-TRSQFLAIAARYFAHGAITLEPLVTA 196
 Db 132 P-----TQGAMPAPASA--FQRAGGVLYASHLQSFLEVSYRLRH----LAQP 174

RESULT 13
 US-09-950-473-2
 ; Sequence 2, Application US/09950473
 ; Patent No. US2002015148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sarkar, Casim
 ; APPLICANT: Lauffenburger, Douglas
 ; TITLE OF INVENTION: G-CSF Analog Compositions and Methods
 ; FILE REFERENCE: 01017/37732
 ; CURRENT APPLICATION NUMBER: US/09/950,473
 ; CURRENT FILING DATE: 2001-09-10
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-950-473-2

Query Match 7.4%; Score 76.5; DB 10; Length 174;
 Best Local Similarity 29.6%; Pred. No. 0.86; Mismatches 17; Indels 27; Gaps 7;
 Matches 34; Conservative 17; Mismatches 17;

Qy 90 CLQRIRGAFYKHLDSDFK-GEPALPDSPMEQLHTS-----LLGSQLQ 137
 Db 74 CLSQHSGLFLYQGLQA--LEGISPEGLPTLDLQDADFTTIWQMEELGMAPAQ 131

Qy 138 PEDHPRETO-QMPSLSSQQWQPLRSKIL-TRSQFLAIAARYFAHGAITLEPLVTA 196
 Db 132 P-----TQGAMPAPASA--FQRAGGVLYASHLQSFLEVSYRLRH----LAQP 174

RESULT 14
 US-10-016-403-1
 ; Sequence 1, Application US/10016403
 ; Patent No. US2002010750A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Holladay, Leslie A.
 ; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
 STREET: 25 West Main Street
 CITY: Madison
 STATE: WI
 COUNTRY: USA
 ZIP: 53701-2236

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/016,403
 FILING DATE: 10-Dec-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/466,610
 FILING DATE: 1995-JUN-06

ATTORNEY/AGENT INFORMATION:
 NAME: Frenchick, Grady J.
 REGISTRATION NUMBER: 29,018
 REFERENCE/DOCKET NUMBER: 8734.28

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-257-2281
 TELEFAX: 608-257-7643

SEQUENCE CHARACTERISTICS:
 LENGTH: 174 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..174
 OTHER INFORMATION: /note= "modified granulocyte-colony stimulating factor"
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-016-403-2

Query Match 7.4%; Score 76.5; DB 12; Length 174;
 Best Local Similarity 29.6%; Pred. No. 0.86;
 Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;

QY 90 CLQRIRQGLAFYKHLLSDIFKG-EPAILLPDSPEQLHTS-----LIGLSQLLQ 137
 Db 74 CLSQLHSGLFLYQGLQA--LEGTSPELGPFLTLQLQDAFATTIQQMEEIGMAPLQ 131

QY 138 PEDHMPRETO-QMPSLSSQQWQPLRSLKILRSQAFIAARYFAHGAATLTERP 191
 Db 132 P-----TQGAMPAPASA--FQRAGGYLVASHLQSFLFLEVSYRLRH---LAQP 174

Search completed: November 20, 2002, 12:00:55
 Job time : 7.63636 secs

RESULT 15
 US-10-016-403-2
 ; Sequence 2, Application US/10016403
 ; Patent No. US2002107505A1

GENERAL INFORMATION:
 ; APPLICANT: Holladay, Leslie A.
 ; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
 ; INCREASE ELECTROTRANSPORT FLUX

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
 ; STREET: 25 West Main Street
 ; CITY: Madison
 ; STATE: WI
 ; COUNTRY: USA
 ; ZIP: 53701-2236

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

Qy 61 EDEETKNNVPRIQEDGDPGLKDNSOFCLORIQLAFYKHLDSIFKGEPLLPSD 120
Db 61 EDEETKNNVPRIQEDGDPGLKDNSOFCLORIQLAFYKHLDSIFKGEPLLPSD 120

RESULT 3
US-09-122-443-5
; Sequence 5, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-5

Query Match 34.3%; Score 356; DB 3; Length 102;
Best Local Similarity 72.3%; Pred. No. 9.1e-33;
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 90 CLORIROGLAYKHLDSDFIKGEPALLPSPMELHTSLLGLSOLLOPDHPRETOOMP 149
Db 2 CLQRINGLVLYEKLGSDIFGPSPVGOLHASLGLRQLQPEGHHWETEQTP 61

Query Match 34.3%; Score 356; DB 3; Length 190
Best Local Similarity 72.3%; Pred. No. 9.1e-33;
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 150 SLSQQWQPLRSKILRSQAFIAARVFAGAATL 190
Db 62 SPSPSQFWQRLRLKLRSLQAFIAARVFAGAATLSQ 102

RESULT 4
US-09-499-148-5
; Sequence 5, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: Sorens, William
; APPLICANT: Steahl, Mark L.
; APPLICANT: Sehra, Jasbir S.
; APPLICANT: Au, Guang-Yi
; APPLICANT: McConagh, Thomas E.
; APPLICANT: Yul Hwang, Al
; APPLICANT: Hong, Jin
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-052780US1

Qy 1 MLDCRAVIMWLPVTOGLAVPRSSSPDWAOCQQLSRNLCMLAWNAAHAPAGHMLLRE 60
Db 1 MLGSRAVMWLLPMLPTAQGRAVPGSSPAWCQQLSRNLCMLAWSAIPVGIMD-GREE 59

Qy 61 EDEETKNNVPRIQEDGCDPGLKDNSOFCLORIQLAFYKHLDSIFKGEPLLPSD 120
Db 60 GDEETKNDVPHIOQCDGCDPGLKDNSOFCLORIQLAFYKHLDSIFKGEPLLPSD 119

Qy 121 PMEQLHTSLLGLSQLQEPHPRTOQMPSLSSQQWQPLRSKILRSQAFIAARV 180
Db 120 PVQHAASLGLSQLQEPHWTQFISLSPSOPWQPLRSKILRSQAFIAARV 179

Qy 181 FAHGAATLT 189

CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIORITY FILING DATE: 1997-4-28 AND 1996-8-16
; SEQ ID NO: 9
; SOFTWARE: PatentIn version 3.0
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-499-148-5

Query Match Score 112; DB 4; Length 162;
Best Local Similarity 27.7%; Pred. No. 7.9e-05;
Matches 39; Conservative 22; Mismatches 50; Indels 30; Gaps 6;

Qy 59 EEEDE-----ETKNNVPRIOEDGCDPQLKDNNSQFCLQRIRGAFYKHLLD--S 107
Db 27 EKNDECNSKETLAENKLKPMEEDGCFQSFGF--NQAICLIRTAGLEQIYDLYQ 106

Qy 108 DIFKGEPALLPDSPMEQLHTSLLGLSQLQ-----PEDIHPRETQOMPSLSSQQWQ 158
Db 85 NEFEGN----QETMELQSSIRTLIQILKEKIALGITTPATH--IDMLERKMQSSNEWV 136

Qy 159 RPLRSKILRSQFLAIAAR 179
Db 137 KNAKVITLSSLNFQFSLR 157

RESULT 5
OS-09-122-443-13
; Sequence 13, Application US/09122443
; Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Baran, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
ZIP: 94304-1104
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/1122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chin, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)4852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 184; amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLCULE TYPE: Peptide

Query Match 10.8%; Score 112; DB 3; Length 184;

Best Local Similarity 27.7%; Pred. No. 7.9e-05;
Matches 39; Conservative 22; Mismatches 50; Indels 30; Gaps 6;

Qy 59 EEEDE-----ETKNNVPRIOEDGCDPQLKDNNSQFCLQRIRGAFYKHLLD--S 107
Db 49 EKNDECNSKETLAENKLKPMEEDGCFQSFGF--NQAICLIRTAGLEQIYDLYQ 106

Qy 108 DIFKGEPALLPDSPMEQLHTSLLGLSQLQ-----PEDIHPRETQOMPSLSSQQWQ 158
Db 107 NEFEGN----QETMELQSSIRTLIQILKEKIALGITTPATH--IDMLERKMQSSNEWV 158

Qy 159 RPLRSKILRSQFLAIAAR 179
Db 159 KNAKVITLSSLNFQFSLR 179

RESULT 6
US-09-499-148-2
; Sequence 2, Application US/09499148
; Patent No. 64,61604
GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; STAHL, MARK L.
; SEEHRA, JASBIR S.
; XU, GUANG-YI
; MCCONAGH, THOMAS E.
; YU, HSIANG AI
; HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-03278USCI
; CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 08/941,035 AND 60/024,115
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOs: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 162
; TYPE: PPT
; ORGANISM: Bos taurus
US-09-499-148-2

Query Match Score 10.0%; Score 104; DB 4; Length 162;
Best Local Similarity 26.8%; Pred. No. 0.00053;
Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;

Qy 59 EEEDE-----ETKNNVPRIOEDGCDPQLKDNNSQFCLQRIRGAFYKHLLD--S 107
Db 27 EKNDECNSKETLAENKLKPMEEDGCFQSFGF--NQAICLIRTAGLEQIYDLYQ 84

Qy 108 DIFKGEPALLPDSPMEQLHTSLLGLSQLQ-----PEDIHPRETQOMPSLSSQQWQPL 161
Db 85 NEYEGRQENVRD----LRKNTRLQIQLKOKIADLITTPATNTDLERKMQSSNEWVKA 139

Qy 162 LRSKILRSQFLAIAAR 179
Db 140 KILLURNLLENFLQFSLR 157

RESULT 7
US-09-499-148-3
; Sequence 3, Application US/09499148
; Patent No. 64,61604
GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; STAHL, MARK L.
; SEEHRA, JASBIR S.
; XU, GUANG-YI
; MCCONAGH, THOMAS E.
; YU, HSIANG AI
; HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USCI

CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIORITY APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIORITY FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 3
; LENGTH: 166
; TYPE: PRT
; ORGANISM: *Felis catus*
; US-09-499-148-3

Query Match 9.9%; Score 103; DB 4; Length 166;
Best Local Similarity 24.8%; Pred. No. 0.00071; Mismatches 55; Indels 32; Gaps 6;

Matches 38; Conservative 28; Mismatches 55; Indels 32; Gaps 6;

52 GHMNLREDE-----ED-----ETKNNVPRIQEDGCDPQGLKDONSQFLQRQL 98
16 GKISALKKEMCDNYNKCDSEKLAENNLNLPAKERAEGCFQSFGF - NQECLMRITGL 73

99 AFYKHLD--SDIFKGEPALLPSPMEQLPQHLSLGLSOLQPEDHPRETOQMP-----149
74 QEFQIYLKFLQDKYEGD-----BENAKSVYSTSTNVLLQMLKKRGKGNDEVTTPVPTVEVG 128

150 ---LSLSSQQWQRPLRSKILRSQAFALAAAR 179
129 LQAKLQSQEWLRHTTHTLRLDFLQFLSR 161

Db 127 ALLTD-----KLESKEWLRTKTFQFLKSLEPEFKVILR 161

RESULT 8
US-09-499-148-9
; Sequence 9, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USC1
; CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIORITY APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIORITY FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 9
; LENGTH: 166
; TYPE: PRT
; ORGANISM: *Sus scrofa domestica*
; US-09-499-148-9

Query Match 9.9%; Score 100; DB 4; Length 166;
Best Local Similarity 25.0%; Pred. No. 0.0015; Mismatches 57; Indels 38; Gaps 5;

Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps 5;

52 GHMNLREDE-----ETKNNVPRIQEDGCDPQGLKDONSQFLQRQL 98
16 GKISALKKEMCDNYNKCDSEKLAENNLNLPAKERAEGCFQSFGF - NQECLMRITGL 73

99 AFYKHLD--SDIFKGEPALLPSPMEQLPQHLSLGLSOLQPEDHPRETOQMP---150
74 VEFQIYLKFLQKEWSNKG-----VEAQVISTRALIQTLRQKGKNPDRATTNPPTT 125

151 ---LSSQQWQRPLRSKILRSQAFALAAAR 179
126 NAGLDDKLOSSNEWMKNTKILLLSLDFQSLR 161

RESULT 9

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 14;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

RESULT 11
; Sequence 96; Score 96; DB 3; Length 188;
; Best Local Similarity 25.5%; Pred. No. 0.0052;
; Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

Query Match 9.2%; Score 96; DB 4; Length 211;
; Best Local Similarity 25.5%; Pred. No. 0.0062;
; Matches 4; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCMLAANAHAPAGHMNLREEEDEETKNN - VPRIQCEDGDPQGLKDNDNSQFCLQ 92
; Db 64 EMRKELC - - - NGNSDC - MN - - - NDDALAENNLKLPETQRNDCYCTGY - - - NOEICLL 111
; QY 93 RIRGQLAFKHLLD - - - SDIFKGEPALLP - - - - - DSpMEQLHTSSL - - - - - GLSQ 134
; Db 112 KISSGLLEYHSYLEYMKNNKLKDARVLQRDTETLIHFNQEVKDLHKIVLPTPSN 171
; QY 135 LLQPEDHPRETOQMPSSQWORPLRSKILRSQAFIAAR 179
; Db 172 ALLTD - - - - - KLESQKEWLRTKTIQFLIKSLEEFKVTLR 206

RESULT 12
; Sequence 6; Application US/08209182C
; Patent No. 5545537
; GENERAL INFORMATION:
; APPLICANT: Skelly, Susan M.
; APPLICANT: Tackney, Charles T.
; APPLICANT: Shouwaert, John N.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: Cysteine depleted IL-6 Mutants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/209,182C
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/724,698
; FILING DATE: 02-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: SKE-1-PD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2554
; INFORMATION FOR SEQ ID NO: 6;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

RESULT 13
; Sequence 8; Application US/08097869
; Patent No. 6204364
; GENERAL INFORMATION:
; APPLICANT: Todaro, George J.
; APPLICANT: Rose, Timothy M.
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZTIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,869
; FILING DATE: 30-AUG-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,178
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 8;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-097-869-8

RESULT 13
CT-US92-05612-6
Sequence 6, Application PC/TUS9205612
GENERAL INFORMATION:
APPLICANT: Shelly, Susan M.
APPLICANT: Stouwaert, John N.
APPLICANT: Tackney, Charles T.
TITLE OF INVENTION: Cysteine Depleted IL-6 Mutants
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05612
FILING DATE: 19920702
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Peit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: SKE-1-PT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05612-6

Query Match 8 9%; Score 92.5; DB 5; Length 186;
Best Local Similarity 25.7%; Pred. No. 0.013; Gaps 4;
Matches 36; Conservative 22; Mismatches 61; Indels 21;

Qy 53 HMMNLREEDDEETKNNVPRIOCEDCDPQGLKDNSQCLQRGFLAFYKHLLSDIFKG 112
Db 50 NMSESSKEALAENNUNLPKAEKDCFOSEF--NEETCLVKITIG-----LLEFEVYVE 101

Query Match 8 9%; Score 92.5; DB 5; Length 186;
Best Local Similarity 25.7%; Pred. No. 0.013; Gaps 4;
Matches 36; Conservative 22; Mismatches 61; Indels 21;

Qy 102 TPPRPESEEQARAVQMSTKVLIQLQQNWLQ 161
Db 100 PLLRSKILRSQAFIAAR 179

Query Match 8 9%; Score 92.5; DB 5; Length 186;
Best Local Similarity 25.7%; Pred. No. 0.013; Gaps 4;
Matches 36; Conservative 22; Mismatches 61; Indels 21;

Qy 160 PLLRSKILRSQAFIAAR 179
Db 162 DMTHLILRSKFEFLSSLR 181

RESULT 14
US-09-499-148-6
Sequence 6, Application US/09499148
GENERAL INFORMATION:
APPLICANT: SOMBERS, WILLIAM
APPLICANT: STAHL, MARK L.
APPLICANT: SEEHRA, JASBIR S.
APPLICANT: MCCONAGH, THOMAS E.
APPLICANT: GUANG-YI
APPLICANT: QI, GUANG-YI
Patent No. 6461604
GENERAL INFORMATION:
APPLICANT: SOMERS, WILLIAM
APPLICANT: STAHL, MARK L.
APPLICANT: SEEHRA, JASBIR S.
APPLICANT: MCCONAGH, THOMAS E.
APPLICANT: GUANG-YI
APPLICANT: QI, GUANG-YI

RESULT 15
US-09-487-792-14
Sequence 14, Application US/09487792
GENERAL INFORMATION:
Patent No. 6433145
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Keratinocyte Derived Interferon
FILE REFERENCE: PF4BSP1
CURRENT APPLICATION NUMBER: US/09/487,792
CURRENT FILING DATE: 2000-01-20
EARLIER APPLICATION NUMBER: 60/093,543
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: PCT/US99/16424
EARLIER FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14

Query Match 8 6%; Score 89; DB 4; Length 212;
Best Local Similarity 22.0%; Pred. No. 0.038; Gaps 7;
Matches 39; Conservative 27; Mismatches 71; Indels 40;

Qy 75 EDGCDPQGLKDNSQCLQRGFLAFYKHLL-SDIFKGEPALPDSPMEQLHTSLGL 132
Db 74 YLDGTSALKET-----CNK-SMCSESSKEALA-----ENNLNPKMAK 97

Query Match 8 6%; Score 89; DB 4; Length 212;
Best Local Similarity 22.0%; Pred. No. 0.038; Gaps 7;
Matches 39; Conservative 27; Mismatches 71; Indels 40;

Qy 98 EDGCDPQGLKDNSQCLQRGFLAFYKHLL-SDIFKGEPALPDSPMEQLHTSLGL 132
Db 97 EDGCDPQGLKDNSQCLQRGFLAFYKHLL-SDIFKGEPALPDSPMEQLHTSLGL 132

Query Match 8 6%; Score 89; DB 4; Length 212;
Best Local Similarity 22.0%; Pred. No. 0.038; Gaps 7;
Matches 39; Conservative 27; Mismatches 71; Indels 40;

Qy 133 SQLQPE-----DHPRETOQMPSLSSQQWQRPLRSKTRLSQFLAIAAR 179
Db 151 TQFLQKAKNLDAITTPDPTTNASLLTKLQAQNOWLQDMTTHLIRSFKEFLOSSLR 207

Search completed: November 20, 2002, 12:00:13

Wed Nov 20 13:29:03 2002

us-09-658-699-4.ra1

Page 7

Job time : 13.2182 secs

